

Quality: 810.00 Length: 157
 Ratio: 5.192 Gaps: 0
 Percent Similarity: 99.464 Percent Identity: 99.464
 alignment block:
 uc-09-479-862-1 v us0909
 Align seq 1/1 to: F15793 from: 1 to: 471
 1 TyrPhenylalanylserineValIleAsnLeuAspAs 17
 1 TACTTTCGTAAGCTTGAATTAATATCATAGAGAAATTCGATCA 50
 17 pellaValleuPhenylleAspSerValIleAsnLeuAspMet 44
 51 CCAAGTTCCTCTATATGATAGAGAAATTCGATTAATTCGATCA 100
 44 hrAspSerAspTyrAsnLeuValIleAsnLeuAspMet 50
 101 CTGATTCGATGATAGAGAAATTCGATTAATTCGATTAATTCGAT 157
 51 MetTyrAspSerValIleAsnLeuValIleAsnLeuAspMet 67
 151 ATCTATAAGAGATAGAGAGATAGAGATAGAGATAGAGATAGAGAT 200
 67 sYsclulalylser***LeuSerValIleAsnLeuAspMet 84
 201 GTGATAGAGAAATTCGATTAATTCGATTAATTCGATTAATTCGAT 250
 84 ysluMetAsnProProAspAsnLeuValIleAsnLeuAspMet 100
 251 AAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAG 300
 101 PhosphoValSerValProGlyHisAspSerValIleAsnLeuAsp 117
 301 TCTTTCAGAGAGATGCTGAGAGAGATGAGATGAGATGAGATGAGAT 350
 117 rSerSerTyrGlyGlyTyrPhenylalanylserValIleAsnLeuAsp 134
 351 TTTATCATAGAGAGATGCTGAGAGATGAGATGAGATGAGATGAGAT 400
 134 leuYsclulalylserValIleAsnLeuValIleAsnLeuAspMet 150
 401 TTAAGATCATTTTGAAGAAATGAGATGAGATGAGATGAGATGAGAT 450
 151 PhosphoValSerValProGlyHisAspSerValIleAsnLeuAsp 167
 451 TTTATCATAGAGAGATGCTGAGAGATGAGATGAGATGAGATGAGAT 471

seq_name: em_pat:E12009
 seq_documentation_block:
 ID: E12009 standard, RRA, RRM, 471 bp
 XX A: E12009
 XX SV: E12009.1
 XX 07-01-1997 (rev. 5.2, created)
 ID 02-SEP-2000 (rev. 65, last updated, Version 2)
 XX cDNA encoding human polypeptide which induces interferon gamma product in
 DE immunocompetent cell.
 XX 2P: 1997-2000 A/1
 XX Homo sapiens (human)
 ca Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 ca Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX (1)
 RN 1-471
 RP Kurikata T., Taniguchi M., Kono K., Fujimori M.

"IMPERIAL ANTI BODY"
 ID: E12009 standard, RRA, RRM, 471 bp
 XX A: E12009
 XX SV: E12009.1
 XX 07-01-1997 (rev. 5.2, created)
 ID 02-SEP-2000 (rev. 65, last updated, Version 2)
 XX cDNA encoding human polypeptide which induces interferon gamma product in
 DE immunocompetent cell.
 XX 2P: 1997-2000 A/1
 XX Homo sapiens (human)
 ca Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 ca Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX (1)
 RN 1-471
 RP Kurikata T., Taniguchi M., Kono K., Fujimori M.

alignment scores:
 Quality: 810.00 Length: 157
 Ratio: 5.192 Gaps: 0
 Percent Similarity: 99.464 Percent Identity: 99.464
 alignment block:
 uc-09-479-862-1 x E12009
 Align seq 1/1 to: E12009 from: 1 to: 471
 1 TyrPhenylalanylserineValIleAsnLeuAspAs 17
 1 TACTTTCGTAAGCTTGAATTAATATCATAGAGAAATTCGATCA 50
 17 pellaValleuPhenylleAspSerValIleAsnLeuAspMet 44
 51 CCAAGTTCCTCTATATGATAGAGAAATTCGATTAATTCGATCA 100
 44 hrAspSerAspTyrAsnLeuValIleAsnLeuAspMet 50
 101 CTGATTCGATGATAGAGAAATTCGATTAATTCGATTAATTCGAT 157
 51 MetTyrAspSerValIleAsnLeuValIleAsnLeuAspMet 67
 151 ATCTATAAGAGATAGAGAGATAGAGATAGAGATAGAGATAGAGAT 200
 67 sYsclulalylser***LeuSerValIleAsnLeuAspMet 84
 201 GTGATAGAGAAATTCGATTAATTCGATTAATTCGATTAATTCGAT 250
 84 ysluMetAsnProProAspAsnLeuValIleAsnLeuAspMet 100
 251 AAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAGAGATAG 300
 101 PhosphoValSerValProGlyHisAspSerValIleAsnLeuAsp 117
 301 TCTTTCAGAGAGATGCTGAGAGAGATGAGATGAGATGAGATGAGAT 350
 117 rSerSerTyrGlyGlyTyrPhenylalanylserValIleAsnLeuAsp 134
 351 TTTATCATAGAGAGATGCTGAGAGATGAGATGAGATGAGATGAGAT 400
 134 leuYsclulalylserValIleAsnLeuValIleAsnLeuAspMet 150
 401 TTAAGATCATTTTGAAGAAATGAGATGAGATGAGATGAGATGAGAT 450
 151 PhosphoValSerValProGlyHisAspSerValIleAsnLeuAsp 167
 451 TTTATCATAGAGAGATGCTGAGAGATGAGATGAGATGAGATGAGAT 471

FT met_peptide 1..471 /organism: Artificial gene
 FT product human IL18 like protein
 FT location/qualifiers 1..471

FEATURES

source

1..471 /organism: "unidentified"

36..87..4 "accession: 32644"

BASE COUNT 166 a 80 c 86 g 149 t

ORIGIN

alignment_scores:

Quality: 782.00 Length: 157
 Ratio: 5.046 Gaps: 0
 Percent Similarity: 98.726 Percent Identity: 98.089

alignment_block:

US 09 479-862-1 x E17146

Align seq 1/1 to: E17146 from: 1 to: 471

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1 TyrPheGlyTyrLeuGlnSerValLeuArgAsnLeuAsnAs 17
   |||||
1 TACTTTGGGAAGCTTCAATCTAAATTAATAGCTATAGAGAAATTTGAAATGA 50
   |||||
17 pGlnValLeuPheLeuAspGlnMetLysAspProGlnPheGlnAspMet 44
   |||||
51 GCAAGTCTGCTGATGAGTAAAGGAAATGAGGCTCTATATGAAATATA 100
   |||||
44 hrAspSerAspCysAlaAspAsnAlaProAlaThrLeuPheLeuLeuSer 50
   |||||
101 CTGATTTGACTCTAGATATAAATAGTAACTGCGGAGTATATTTATTATAAA 150
   |||||
51 MetTyrTyrAspSerGlnIleArgAlaGlyMetAlaValThrLeuSerValIle 67
   |||||
151 ATGTAATAAGATAGTACGCTAGAGGTAAGGCTGTAAATATCTCTGTTGAA 200
   |||||
67 SCysGlnLysIleSer***LeuSerCysGlnAsnLysIleLeuSerPheLeu 84
   |||||
201 GTCTGAGAGAAATTTGAAATCTCTGAGTCTAGAGTAAAGGAAATATCTCTTAA 250
   |||||
84 ySGlnMetAsnProProAspAsnIleLysAspIleLysSerAspIleLeu 100
   |||||
251 AGCAATATGAAATCTCTGTAATACATCTAAAGATACATAAAAGTCAATATA 300
   |||||
101 PhePheGlnArgSerValProGlyHisAspAsnLysMetGlnPheGlnGlu 117
   |||||
301 TTCTTCAGAGAAAGTGTCCAGAGCAATGATAAATAAGATGCAATTTGAATC 350
   |||||
117 rSerSerTyrGlnGlyTyrPheLeuAlaCysGlnLysGlnArgAspLeu 134
   |||||
351 TTCAATATAAGAAAGATATTTTATATCTGAGAGAAAGTACAGATATTT 400
   |||||
134 heLysLeuIleLeuLysGlnAspGlnIleGlnGlyAspArgSerIleMet 150
   |||||
401 TTAATCTCATTTTGAAGAAAGAGATGAAATTTGAGGATATAGATCTATAAAT 450
   |||||
151 PheThrValGlnAspGlnAsp 157
   |||||
451 TTCAATCTTCAAAAGTAAATAC 471

```



101 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 117
 117 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 133
 485 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 151
 117 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 167
 435 TTTATCAACAGAGATACCTTTGAGTCTGAGGAGGAGGAGGAGGAGGAG 481
 134 helysleuileleuylslysschlaaspelidactylasparsethomo 150
 485 TTAAGATCATTTGAAAGAAAGAGAGAGAGATGCGGAGATAGATATAGG 534
 151 PheThrValCysAspGluAsp 157
 535 TTTACTGTTCAAAAAGAGAGC 555

seq_name: 555 us-09-479-862-1.p2n.rng (100 bp) (100 bp) (100 bp)

seq_documentation_block:

id: AAC62200 standard: DNA: 582 bp

ac: AAC62200:

ti: 06-MAR-2001 (first entry)

de: cDNA encoding a human IL-18 with a caspase-8 cleavage site.

kw: Protease cleavage site; caspase 1; interleukin 18; IL-18; protease; ss.

os: Synthetic.

xx: Homo sapiens.

xx: W0200041748 A2.

xx: 19-OCT 2000.

xx: 13-APR-2000; 2000W001100220.

xx: 13-APR-1999; 99FL012427.

xx: (YEDA) YEDA RES & DEV Co LTD.

xx: Rubinstein M, Liu R, Novick D, Binarello C, Graber P;

xx: WP1; 2001 056-1370

xx: P-PSNB; AAB30541.

xx: Preparation of biologically active molecules from its inactive

xx: precursors, comprises mutating their native cleavage site to a site

xx: capable of being cleaved by protease and cleaving the mutated molecule

xx: .

xx: Disclosure: Flt 8a-b; 40pp; Endlish.

xx: The present sequence encodes a human pro-interleukin 18 (IL 18)

xx: with a caspase 8 cleavage site. The natural human sequence of IL 18

xx: was mutated to a site susceptible to cleavage by a common protease.

xx: The specification describes a method for the preparation of biologically

xx: active molecules from their biologically inactive precursors. The method

xx: comprises mutating the native cleavage site to a site capable of being

xx: cleaved by a protease and cleaving the mutated molecule to yield the

xx: active compound. The method is especially used to produce active

xx: cytokines, such as IL 18.

xx: Sequence 582 bp; 205 A; 96 C; 111 G; 170 T; 0 other.

alignment_block:

us-09-479-862-1 & AAC62200

align: seq 171 to: AAC62200 frame: 1 to: 592

1 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 151

117 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 133

109 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 156

17 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 144

159 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 167

54 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 56

209 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 254

117 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 133

259 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 308

67 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 84

309 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 358

84 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 100

359 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 408

101 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 117

409 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 458

117 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 134

459 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 508

134 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 150

509 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 558

151 PhePheCysArgSerValThrGlyHisAspArgLysThrCysPheCysG 157

559 TTTTTCAGAGAAAGTCTGACCAATATATAAATAAGAGTAAATTCGAAAT 579

seq_documentation_block:

id: AAC62200 standard: DNA: 1101 bp.

ac: AAC62200:

xx: 15 JAN 1998 (first entry)

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

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xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

xx: Interferon gamma inducing factor-2 (IGIF-2) cDNA.

PR	29-DEC-1995:	95US 0366A/.
XX	(INV.) INTERMARK INC.	
PFA	Cocks BC, Coleman R, Hawkins PR:	
XX	WPI: 1997-363677/43,	
PR	PFS08; AAW27047	
PR	Noel interferon gamma inducing factor 2 used to screen for compounds to diagnose, treat or prevent tissue damage associated with inflammation	
PT	claim 2; Page 46; 60pp; English.	
PS	This LMA sequence encodes interferon gamma inducing factor 2 (IGIF-2) probes derived from the nucleic acid sequence can be used to participate in the expression of IGIF-2 in conditions that are associated with inflammation or aberrant expression of IGIF-2, the protein can be used to screen for compounds that interact with IGIF-2, such as antibodies, antagonists or other inhibitors (especially ribozymes and antisense sequences) of IGIF-2 expression or activity. The probe also can be used to diagnose, prevent or treat IGIF-2 induction or proliferation, differentiation or maturation of monocytes or lymphocytes, especially in relation to tissue damage associated with inflammation.	
XX	Sequence 1101 BQ7436.A; 241 C; 238 S; 276 F; 3 other;	
SQ		

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alignment_scores:
  quality: 811.00      Length: 167
  Ratio: 5.166        Gaps: 0
  Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
  05-09-479_862_1 & 55174_667
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  Align seq 1/1 to: AAT74987 from: 1 to: 1101
  1  TTTPhoGlySerSerGluSerGlySerGluValGluAlaValGluGluGluGluGlu 17
  11111111111111111111111111111111111111111111111111111111
  412 TACATTGGGAAAGGTTCGAATTTAAATATGATGATGATGATGATGATGATGATG 461
  17 TTTGluValGluPheGluGluAspGluGluGluGluGluGluGluGluGluGluGlu 41
  1111111111111111111111111111111111111111111111111111111
  462 CCAAGGCTCTCTTCATTCATCACTCAAGGAAATCAAGGCTCTCTTCATTCATCA 413
  34 TrpAspSerAspGlySerGluGluGluGluGluGluGluGluGluGluGluGluGlu 50
  1111111111111111111111111111111111111111111111111111111
  412 CTGATTCCTGACTGATGAGATAAATGAGCTCGAGACATAATTAATTAATGAT 461
  51 MetTyrGlySerAspSerGluProGluGluGluGluGluGluGluGluGluGluGlu 47
  1111111111111111111111111111111111111111111111111111111
  462 ATGATTAAGGATAGCGAGGCTATGAGGATAGGCTGAGGCTATGCTGAGGATG 513
  67 SerGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 84
  1111111111111111111111111111111111111111111111111111111
  612 GTGGAGGAAAAATTTAAATCTCTCTCTGTTGGAGAGAAAAATATTCCTTTAA 661
  84 GlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 109
  1111111111111111111111111111111111111111111111111111111
  662 AATGAAATGAATCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATG 611
  101 PhePheGluTrpAspSerValProGluGluGluGluGluGluGluGluGluGluGlu 117
  1111111111111111111111111111111111111111111111111111111
  612 TTTCTTCATGAGAGGCTCTCTCTGATGATGATGATGATGATGATGATGATGATG 661
  117 SerSerTyrGluGluTyrGluGluGluGluGluGluGluGluGluGluGluGluGlu 144
  1111111111111111111111111111111111111111111111111111111
  662 TTTATGATATGATGAGATATATCTCTCTCTGATGATGATGATGATGATGATGAT 711
  134 MetGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 150
  1111111111111111111111111111111111111111111111111111111

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[illegible][illegible]

US-09-479-862-1 x AAV-5463

Align seq 17 x AAV-5463 17 x AAV-5463

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1 TyrPheGlyLysIleuValLysAspSerValIleValAspIleuAsnAs 17
|||||
543 TACTTTAGAAAGCTCAATTAAGATATAGAGTAAAGAAATTTGAAAGAA 542
17 pGluValLeuPheIleAspIleuGlyAsnAlaGlnProLeuPheGluAspMet 44
|||||
594 CCAAGTCTCTTCATATGAGCAAGAAATGAGATGATATTTGAAAGATATCA 642
24 LeuAspSerAspGlnAspAspAlaProAspIleuGlyAspIleuGlySer 60
|||||
643 CTGATCTGACGTGATAGATAAAGTACAGCAAGACATATTTATATTAAGT 692
51 MetTyrLysAspSerGlnProLeuPheGluAspIleuValIleSerValIle 67
|||||
693 ATGATATAAGATATGATCAAGCTGACAGTATAGCTGTGTAATATATCTGCA 742
67 scysGluLysIleSer***LeuSerTyrGluAspLysIleIleSerPheL 84
|||||
743 GGTGAGAAAAATTCACATCTCTCTCTCTGAGAAATATTTCTCTCTTCA 792
84 ysgIleuMetAspProLeuAspAsnIleGlyAspIleuLysSerAspIleu 100
|||||
793 AGCAAAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 842
101 PhePheGlnArgSerValProGlyIleuAspAspLysMetGluPheGluSe 117
|||||
843 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 892
117 rSerSerTyrGlyLeuTyrPheLeuAlaTyrGlySerGluAspIleu 134
|||||
893 TTATATATATGAGAGGATATTTTAGCTTCTGAGAAAAAGAGAGAGATTT 942
134 heLysIleuIleLeuLysGlySerGluAspIleuValAspArgSerIleMet 150
|||||
943 TTAAATTCATTTTCAAAAAAGAGATGAAATGAGGATATATATATATATG 992
151 PheIleValGluAsnGluAsp 157
|||||
993 TTCACCTGTTCAAAACGAAGAC 1013

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seq_name: 272573: 479-862-1: us-09-479-862-1: AAV-5463

seq_documentation_block:

ID: AAT32411; standard; cDNA to mRNA, 471 bp.

XX AAT32411;

XX Ac

XX D1 29-SEP-1996 (first entry)

XX DE Human interferon gamma inducer protein cDNA.

XX KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;

XX KW anti-tumour; antibacterial; immunoregulatory; adoptive immunotherapy;

XX KW therapy; cancer; ds.

XX OS Homo sapiens.

XX FN EF0712931-A2.

XX PU 22-MAY-1996

XX XX 10-NOV-1995; 95JP-0408055

XX XX 29-SEP-1995; 95JP-0274988

XX XX 15-NOV-1994; 94JP-0404203

XX XX 24-FEB-1995; 95JP-0058240

XX XX 10-MAR-1995; 95JP-0078357

XX XX 18-SEP-1995; 95JP-0262062

XX

12 cDNA / mRNA/EST sequence: AAT32411

XX 12 cDNA / mRNA/EST: Fujita T, Ezime T, H. Komura H,

XX Taniguchi M, Tanimoto T, Torioka K, Ushio S;

XX WPI; 1996-252837/26.

XX E-Seq: AAG94564.

XX DNA encoding interferon gamma protein, inducing polypeptide, used to treat and prevent, e.g., viral disease, malignancies and immune disorders

XX EMBL: D-911, EMB: 28; 48pp; English.

XX A cDNA clone (AAT32411) codes for a novel human protein (AA32411) that induces interferon gamma (IFN gamma) protein by immunocompetent cells. It was isolated as a phage DNA clone from a human liver library per amplification of the sequence (see also AAT32409-10) and expressed in Escherichia coli XL-1 Blue MRF'kan allowed protein of recombinant inducer protein. This was used to construct hybridoma H 1, which produced anti-IFN gamma inducer protein monoclonal antibody. H 1A8 is useful in the detection and purification of the inducer protein (see also AAG94554).

XX Sequence 471 bp; 166 A; 76 C; 88 G; 140 T; 1 other;

alignment_score:

quality: 810.00 Length: 157

Ratio: 5.192 Gaps: 0

Percent similarity: 99.63 Percent identity: 99.63

alignment_block:

US 09-479-862-1 x AAT32411

Align seq 1/1 to: AAT32411 From: 1 to: 471

1 TyrPheGlyLysIleuValLysAspSerValIleValAspIleuAsnAs 17

|||||

1 TACTTTAGAAAGCTCAATTAAGATATAGAGTAAAGAAATTTGAAAGAA 50

17 pGluValLeuPheIleAspIleuGlyAsnAlaGlnProLeuPheGluAspMet 44

|||||

51 CCAAGTCTCTTCATATGAGCAAGAAATGAGATGATATTTGAAAGATATCA 100

34 LeuAspSerAspGlnAspAspAlaProLeuPheGluAspIleuSer 50

|||||

161 CTGATCTGACGTGATAGATAAAGTACAGCAAGACATATTTATATTAAGT 156

51 MetTyrLysAspSerGlnProLeuPheGlyMetAlaValIleSerValIle 67

|||||

151 ATGATATAAGATATGACAGCTGACAGTATAGCTGTGTAATATCTCTGCAA 200

67 scysGluLysIleSer***LeuSerTyrGluAspLysIleIleSerPheL 84

|||||

201 GTGAGAAAAATTTCAATCTCTCTCTCTGAGAACAAAAATATTCTCTTCA 250

94 heLysIleuIleLeuLysGlySerGluAspIleuValAspArgSerIleMet 100

|||||

251 AGGAAATGAAATCTCTCTGATACATTCAGGATACAAAAAGTGCATCAATA 300

101 PhePheGlnArgSerValProGlyIleuAspAspLysMetGluPheGluSe 117

|||||

401 TCT 450

134 heLysIleuIleLeuLysGlySerGluAspIleuValAspArgSerIleMet 150

|||||

401 TTAAATTCATTTTCAAAAAAGAGATGAAATGAGGATATATATATATATG 450

151 PheIleValGluAsnGluAsp 157

|||||

993 TTCACCTGTTCAAAACGAAGAC 1013

XX A drug containing a polypeptide which induces interferon gamma
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases
 XX
 PS Disclosure: Page 9-10; 12pp; Japanese.
 XX
 CC This sequence encodes a protein which induces interferon gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX
 CC Sequence 471 BP; 166 A; 76 C; 88 G; 140 T; 1 other;

alignment_scores:
 Quality: 810.00 Length: 157
 Ratio: 5.192 Gaps: 0
 Percent Similarity: 53.363 Percent Identity: 53.363

alignment_block:

us-09-479-862-1 x AA: 279

Align seq 1/1 to: AA180209 from: 1 to: 471

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1 TyrPheGlyIysGluSerIysLeuSerValThrArgAsnLeuAspAs 17
1 TACITTCGCAAGCTTGAATCTAAATATACAGACGCAIAGCAAAATTTCAAGGA 50
17 PheValLeuPheGluAspGlyAsnArgProLeuGluPheGluAspMet 34
1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 111
51 CCAAGTTCCTCTTATTGACACAAACAAATCCGATCTATTTGAGGATATGCA 100
34 ArgAspSerAspGlyArgAspAsnLeuArgProLeuGluPheGluAspMet 56
1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 111
101 CTGATCTCTGATCTGATAGATATTAATGCAATCCGACACATATTTATTTATTAAT 150
51 MetTyrLeuAspSerGluProArgGlyMetAlaValThrLeuSerValThr 67
1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 111
151 ALGATATTAAGATATATAGATATTAAGGATATGATGTGATGATATCTGTGAA 200
67 SCysGluAspTyrLeuSer***LeuSerGlySerGluAsnLeuPheGluAspMet 43
1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 111
201 CTGTGCAAAAATTTTCAATATCTCTCTGAGACAAACAAATATTTTCTTTTCA 250
84 YSGluMetAsnProArgAspAsnLeuLeuAspPheIysSerAspLeuThr 300
251 AGCAAAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 350
101 PhePheGluArgSerValProGlyThrAspAsnLeuGluPheGluAspMet 417
401 TTTCTTCACAGCAAGGTGTCAGACACACAGACAGACAGATAAATATGTAATTCGAAT 450
117 TSerSerTyrGluGlyTyrPheLeuAlaCysGluAspGlySerGluAspSer 434
451 TTCAATCAATACAGGATATTTCTAGCTTCTGTAAGAAATATAGAGAGAGATTT 480
134 PheTyrSerLeuLeuLeuTyrLeuAspGluLeuLeuTyrAspArgSerLeuMet 450
401 TTAACATCATTTTGAAGAAACAGCATGATTTGAGGATATGATGATGATGATGATG 450
151 PheThrValThrAsnLeuAsp 157
451 TTCATTCGATCAAAAGAAAC 471

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seq.name: us-09-479-862-1.p2n.rng seq.length: 157

seq.document.alignment_block:

10 AA: 56875 standard. 666, 471 BP.

XX

AC 56875;

XX

13 MAK zoon (first entry)
 XX
 CC DNA encoding a mature protein that induces IFN-gamma production in
 CC antiviral, immunoregulatory, antitumor, viral, bacterial or
 CC immunocompetent cells
 KW
 KW IFN-gamma production; IFN-gamma; immunocompetent cells
 KW antiviral; immunoregulatory; antitumor; antitumor;
 KW IFN-gamma susceptible disease; antibacterial; antitumor;
 KW blood platelet enhancing agent; hepatitis; herpes syndrome; candida
 KW AIDS; bacterial disease; candidiasis; malaria; solid malignant tumor;
 KW renal cancer; mycosis; tumours; chronic granulomatous disease;
 KW blood cell malignant tumor; adult T cell leukaemia;
 KW chronic myelogenous leukaemia; malignant leukaemia; immune disease;
 KW allergy; rheumatism; ss.
 XX
 CC Homo sapiens.

XX
 CC Key: Location/Qualifiers

XX
 CC CDS

XX
 CC /start 1

XX
 CC /stop 471

XX
 CC /note "Xaa is His or Thr"

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 CC /start 1

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 CC /stop 471

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GenCore version 4.5,
Copyright (c) 1998 - Zilon Computer Ltd.

2025年10月20日

Rem on: August 2, 2001, 04:09:18 ; Search time: 0.99.11 Seconds
(without alignments)
0.64.500 Million cool updates/sec

```
Title: US-09-479-H6.2-3  
Perfect score: 145  
Sequence: 1 AAAAGGCGAAATTAATAAATTATTTTGGACCTGTCAGAAC
```

Scoring table: $IDENTITY_NUR$
 Capital 10.0 - Capital 1.0

Searched: 144157 seeds, 774874588 positions
Total number of hits against virus database: 2660314

```
Minimum DB seq length: 0
Maximum DB seq length: 200000000
```

Post-processing: Minimum Match: 0.8
Maximum Match: 1.0
List for first 45 summaries

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840.

[illegible]

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| 43: | cm_007: | 43: | cm_007: |
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| 77: | cm_041: | 77: | cm_041: |
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| 95: | cm_059: | 95: | cm_059: |
| 96: | cm_060: | 96: | cm_060: |
| 97: | cm_061: | 97: | cm_061: |

pred. No. is the number of results predicted by chance to be \geq the score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

| Res:Sil
No. | K | | Length | DB | ID | Accession |
|----------------|-------|-------|--------|----|-------------|--|
| | Score | Match | | | | |
| 1 | 1.45 | 100.0 | 1.45 | 10 | E1564.2 | E1564.2; <i>Escherichia coli</i> |
| 2 | 1.45 | 100.0 | 1.45 | 93 | HS429457.24 | A12767.2; <i>Staphylococcus aureus</i> |
| 3 | 1.45 | 100.0 | 57.9 | 93 | AR06455.2 | AR0645.2; <i>Staphylococcus aureus</i> |
| 4 | 1.45 | 100.0 | 57.9 | 10 | E1560.4 | E1560.4; <i>Escherichia coli</i> |
| 5 | 1.45 | 100.0 | 57.9 | 97 | HS090434 | E1564.4; <i>Escherichia coli</i> |
| 6 | 1.45 | 100.0 | 110.2 | 91 | D49950 | E1564.5; <i>Escherichia coli</i> |
| 7 | 1.45 | 100.0 | 112.0 | 10 | E14759 | E14759; <i>Escherichia coli</i> |
| 8 | 1.45 | 100.0 | 112.0 | 10 | E1564.1 | E1564.1; <i>Escherichia coli</i> |

GenCode version 4.0
Copyright (c) 1994-2000 Capgen Ltd.

Molecule - nucleic search, using sw model

Run on: August 2, 2001, 04:59:58 : Search time: 00:04:38 seconds
(without alignments)
335,964 Million cell updates/sec

Title: US-09-479-862-3
Perfect score: 135
Sequence: 1 AAAAATGGAAATCAATTAAT.....GATGATATGATCTCTACAG 135

Scoring table: IDENTITY_NW
Gapop 10.0, Gapext 1.0

Searched: 10228115 seqs, 4726426760 residues
Total number of hits satisfying chosen parameters: 20456240

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match ok
Maximum Match 100%
Listing first 45 summaries

Database:

EST:

1: db_est11:
2: db_est12:
3: db_est13:
4: db_est14:
5: db_est15:
6: db_est16:
7: db_est17:
8: db_est18:
9: db_est19:
10: db_est20:
11: db_est21:
12: db_est22:
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58: db_est68:
59: db_est69:
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110: db_est120:
111: db_est121:
112: db_est122:
113: db_est123:
114: db_est124:
115: db_est125:
116: db_est126:

117: qb_est148: *
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 120: qb_est151: *
 121: qb_est152: *
 122: qb_est153: *
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 140: qb_est171: *
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 255: qb_est286: *
 256: qb_est287: *
 257: qb_est288: *
 258: qb_est289: *
 259: qb_est290: *
 260: qb_est291: *

Print: No. is the number of results predicted by classifier, and is the score of the result, and is the total score distribution.


```

DE 29-SEP-1996 (first entry)
XX
DE Human interferon-gamma inducer protein cDNA.
XX
XX Interferon-gamma inducer protein (IFN-gamma) and viral, therapeutic,
KW anti-tumor, antibacterial; immunoregulatory; adaptive immunotherapy;
KW therapy; cancer; ds.
XX
XX Homo sapiens.
XX
XX EF712931 A2.
XX
XX 22-MAY-1996.
XX
XX 10-NOV-1995; 95JP-048655.
XX
XX 29-SEP-1995; 95JP-0274988.
XX
XX 15-NOV-1994; 94JP-0404203.
XX
XX 23-FEB-1995; 95JP-0058240.
XX
XX 10-MAR-1995; 95JP-0078357.
XX
XX 18-SEP-1995; 95JP-0262362.
XX
XX (HAYE ) HAYASHIHARA SEIJI/SHO KAZUO.
XX
XX FuPai F., Echaz F., Kanikata I., Furukawa M., Okamura E.
XX Taniuchi M., Tanimoto T., Torioka K., Ushio S.
XX
XX WPI: 1996-252827/26.
XX
XX P-PSDB: AAR94558.
XX
XX cDNA encoding interferon-gamma protein, inducing polypeptide, useful
XX to treat and prevent, e.g. viral disease, malignancies and immune
XX disorders
XX
XX claim 4: Page 41: 48pp; English.
XX
XX A cDNA clone (AA132402) codes for a novel human protein (AAR94558) that
XX induces interferon-gamma (IFN-gamma) protein by immunocompetent cells.
XX the clone was obtd. from a human liver cDNA library in Escherichia
XX coli by screening transformants with a probe based on a murine
XX IFN-gamma inducer protein cDNA (see also AA132459). A full-length
XX sequence is 1958 nt (AA132459). The cDNA can be used for the high yield
XX produ. of IFN-gamma inducer protein, esp. in transformed B cell host
XX cells. The protein is useful as an antiviral, antitumor, antibacterial,
XX immunoregulatory and blood platelet enhancing agent
XX
XX Sequence 471 BP; 166 A; 76 C; 88 G; 140 T; 1 other;
SQ

```

```

DE 29-SEP-1996 (first entry)
XX
DE Human interferon-gamma inducer protein cDNA.
XX
XX Interferon-gamma inducer protein (IFN-gamma) and viral, therapeutic,
KW anti-tumor, antibacterial; immunoregulatory; adaptive immunotherapy;
KW therapy; cancer; ds.
XX
XX Homo sapiens.
XX
XX EF712931 A2.
XX
XX 22-MAY-1996.
XX
XX 10-NOV-1995; 95JP-048655.
XX
XX 29-SEP-1995; 95JP-0274988.
XX
XX 15-NOV-1994; 94JP-0404203.
XX
XX 23-FEB-1995; 95JP-0058240.
XX
XX 10-MAR-1995; 95JP-0078357.
XX
XX 18-SEP-1995; 95JP-0262362.
XX
XX (HAYE ) HAYASHIHARA SEIJI/SHO KAZUO.
XX
XX WPI: 1996-252827/26.
XX
XX P-PSDB: AAR94558.
XX
XX cDNA encoding interferon-gamma protein, inducing polypeptide, useful
XX to treat and prevent, e.g. viral disease, malignancies and immune
XX disorders
XX
XX claim 4: Page 41: 48pp; English.
XX
XX A cDNA clone (AA132402) codes for a novel human protein (AAR94558) that
XX induces interferon-gamma (IFN-gamma) protein by immunocompetent cells.
XX the clone was obtd. from a human liver cDNA library in Escherichia
XX coli by screening transformants with a probe based on a murine
XX IFN-gamma inducer protein cDNA (see also AA132459). A full-length
XX sequence is 1958 nt (AA132459). The cDNA can be used for the high yield
XX produ. of IFN-gamma inducer protein, esp. in transformed B cell host
XX cells. The protein is useful as an antiviral, antitumor, antibacterial,
XX immunoregulatory and blood platelet enhancing agent
XX
XX Sequence 471 BP; 166 A; 76 C; 88 G; 140 T; 1 other;
SQ

```

Search completed: August 2, 2001, 07:17:48
Job time: 86.4 sec

GeneCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

cm nucleic = nucleic search, using sw model

Run on: August 2, 2001, 07:12:24 : Search time 0'09.11 Seconds
(all 6000 alignments)
9061.264 Million cell updates/sec

Title: US-09-479-862 7
Percent score: 2167

Sequence: 1 GAAATGAAATGATGATGAA.....AGTATGAAATGATGATGAT 2167

Scoring table: IDENTITY_NU*

Gapop 10.0 : Gapext 1.0

Searched: 144165 seqs, 773464000 residues

Total number of hits satisfying chosen parameters: 2688414

Minimum db seq length: 6

Maximum db seq length: 20000000

Post-processing: Minimum Match ok

Maximum Match 100%

Fastest First 45 Summaries

Database:

GenBank: *
1: ab_ba1: *
2: ab_ba2: *
3: ab_ba3: *
4: ab_ba4: *
5: ab_ba5: *
6: ab_ba6: *
7: ab_ba7: *
8: ab_ba8: *
9: ab_ba9: *
10: ab_ba10: *
11: ab_ba11: *
12: ab_ba12: *
13: ab_ba13: *
14: ab_ba14: *
15: ab_ba15: *
16: ab_ba16: *
17: ab_ba17: *
18: ab_ba18: *
19: ab_ba19: *
20: ab_ba20: *
21: ab_ba21: *
22: ab_ba22: *
23: ab_ba23: *
24: ab_ba24: *
25: ab_ba25: *
26: ab_ba26: *
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35: ab_ba35: *
36: ab_ba36: *
37: ab_ba37: *
38: ab_ba38: *
39: ab_ba39: *
40: ab_ba40: *
41: ab_ba41: *
42: ab_ba42: *
43: ab_ba43: *

44: cm_001: *
45: cm_002: *
46: cm_003: *
47: cm_004: *
48: cm_005: *
49: cm_006: *
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61: cm_018: *
62: cm_019: *
63: cm_020: *
64: cm_021: *
65: cm_022: *
66: cm_023: *
67: cm_024: *
68: cm_025: *
69: cm_026: *
70: cm_027: *
71: cm_028: *
72: cm_029: *
73: cm_030: *
74: cm_031: *
75: cm_032: *
76: cm_033: *
77: cm_034: *
78: cm_035: *
79: cm_036: *
80: cm_037: *
81: cm_038: *
82: cm_039: *
83: cm_040: *
84: cm_041: *
85: cm_042: *
86: cm_043: *
87: cm_044: *
88: cm_045: *
89: cm_046: *
90: cm_047: *
91: cm_048: *
92: cm_049: *
93: cm_050: *
94: cm_051: *
95: cm_052: *
96: cm_053: *
97: cm_054: *
98: cm_055: *

Prod. No. is the number of results predicted by chance for a given score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | Description |
|------------|--------|-------|-----------|-------------|
| | | Match | Length DB | |
| 1 | 2167 | 100.0 | 2167 | E15646 |
| 2 | 2167 | 100.0 | 28994 | E15653 |
| 3 | 2150.2 | 99.2 | 161920 | AF002502 |
| 4 | 2149.2 | 99.2 | 187516 | AF009648 |
| 5 | 2145.4 | 99.0 | 167069 | AF006783 |
| 6 | 2145.4 | 99.0 | 168922 | AF002007 |
| 7 | 2145.4 | 99.0 | 172059 | AF00815 |
| 8 | 562.2 | 25.9 | 1120 | E14759 |

9 562.2 25.9 1120 19 115641
 10 562.2 25.9 1120 45 111745
 11 560.2 25.9 1102 91 104950
 12 515.2 14.5 98992 91 10000000
 13 515.2 14.5 214466 65 10019224
 14 515.2 14.5 440000 91 10001751
 15 511.6 14.4 110000 65 10018654
 16 511.4 14.4 149464 65 10012411
 17 510.2 14.4 161571 88 10009462
 18 510.2 14.4 162439 68 10024151
 19 510.2 14.4 165675 88 10006646
 20 510.2 14.4 166991 88 10009084
 21 510.2 14.4 168464 22 10011607
 22 507.6 14.2 202914 76 10026555
 23 505.8 13.7 147501 78 10006675
 24 504.6 13.6 164945 64 10016696
 25 503.3 13.5 191953 97 10017395
 26 501.8 13.5 165960 92 10020862
 27 501.4 13.4 154228 89 10015517
 28 501.4 13.4 185679 88 10022534
 29 501.4 13.4 186198 81 10025304
 30 501.4 13.4 187228 71 10024114
 31 501.4 13.4 187544 70 10025444
 32 501.4 13.4 188196 70 10026579
 33 501.4 13.4 189176 70 10026579
 34 501.4 13.4 190176 70 10026579
 35 501.4 13.4 191176 70 10026579
 36 501.4 13.4 192176 70 10026579
 37 501.4 13.4 193176 70 10026579
 38 501.4 13.4 194176 70 10026579
 39 501.4 13.4 195176 70 10026579
 40 501.4 13.4 196176 70 10026579
 41 501.4 13.4 197176 70 10026579
 42 501.4 13.4 198176 70 10026579
 43 501.4 13.4 199176 70 10026579
 44 501.4 13.4 200176 70 10026579
 45 501.4 13.4 201176 70 10026579

ALIGNMENTS

1 115641
 2 111745
 3 104950
 4 10000000
 5 10019224
 6 10001751
 7 10018654
 8 10012411
 9 10009462
 10 10024151
 11 10006646
 12 10009084
 13 10011607
 14 10026555
 15 10006675
 16 10016696
 17 10017395
 18 10020862
 19 10015517
 20 10022534
 21 10025304
 22 10024114
 23 10025444
 24 10026579
 25 10026579
 26 10026579
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 28 10026579
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 35 10026579
 36 10026579
 37 10026579
 38 10026579
 39 10026579
 40 10026579
 41 10026579
 42 10026579
 43 10026579
 44 10026579
 45 10026579

1 115641
 2 111745
 3 104950
 4 10000000
 5 10019224
 6 10001751
 7 10018654
 8 10012411
 9 10009462
 10 10024151
 11 10006646
 12 10009084
 13 10011607
 14 10026555
 15 10006675
 16 10016696
 17 10017395
 18 10020862
 19 10015517
 20 10022534
 21 10025304
 22 10024114
 23 10025444
 24 10026579
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 35 10026579
 36 10026579
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 38 10026579
 39 10026579
 40 10026579
 41 10026579
 42 10026579
 43 10026579
 44 10026579
 45 10026579

[illegible][illegible]

GenCore version 4.5
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OM nucleic nucleic search, using sw mod-1

Run on: August 2, 2001, 07:10:28 : Search time: 4699.11 Seconds
(without alignments)
560,418 hits in 11141 cells updated/s/c

11141
Percent score: 134

Sequence: 1 AATAAGTACGCGGAGGAGTA...AAAAATATTTCTTTAAG 134

Scoring table: IDENTITY NW
Gapop 10.0 / Gapext 1.0

Searched: 1544157 seqs, 773827528 reads

Total number of hits satisfying chosen parameters: 2088414

Minimum DB seq length: 5

Maximum DB seq length: 200000000

Post-processing: Minimum Match: 9K

Maximum Match: 100K

Lasting first 4% summaries

Database:

GenBank: *
1: ab_001: *
2: ab_002: *
3: ab_003: *
4: ab_004: *
5: ab_005: *
6: ab_006: *
7: ab_007: *
8: ab_008: *
9: ab_009: *
10: ab_010: *
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12: ab_012: *
13: ab_013: *
14: ab_014: *
15: ab_015: *
16: ab_016: *
17: ab_017: *
18: ab_018: *
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20: ab_020: *
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22: ab_022: *
23: ab_023: *
24: ab_024: *
25: ab_025: *
26: ab_026: *
27: ab_027: *
28: ab_028: *
29: ab_029: *
30: ab_030: *
31: ab_031: *
32: ab_032: *
33: ab_033: *
34: ab_034: *
35: ab_035: *
36: ab_036: *
37: ab_037: *
38: ab_038: *
39: ab_039: *
40: ab_040: *
41: ab_041: *
42: ab_042: *
43: ab_043: *

44: em_001: *
45: em_002: *
46: em_003: *
47: em_004: *
48: em_005: *
49: em_006: *
50: em_007: *
51: em_008: *
52: em_009: *
53: em_010: *
54: em_011: *
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56: em_013: *
57: em_014: *
58: em_015: *
59: em_016: *
60: em_017: *
61: em_018: *
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68: em_025: *
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71: em_028: *
72: em_029: *
73: em_030: *
74: em_031: *
75: em_032: *
76: em_033: *
77: em_034: *
78: em_035: *
79: em_036: *
80: em_037: *
81: em_038: *
82: em_039: *
83: em_040: *
84: em_041: *
85: em_042: *
86: em_043: *
87: em_044: *
88: em_045: *
89: em_046: *
90: em_047: *
91: em_048: *
92: em_049: *
93: em_050: *
94: em_051: *
95: em_052: *
96: em_053: *
97: em_054: *
98: em_055: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being shown and is derived by analysis of the total score distribution

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Dataset |
|------------|-------|-------|--------|-------|----------|
| 1 | 134 | 100.0 | 134 | 10 | E15643 |
| 2 | 134 | 100.0 | 471 | 10 | E17135 |
| 3 | 134 | 100.0 | 579 | 97 | HS090434 |
| 4 | 134 | 100.0 | 582 | 9 | A0039046 |
| 5 | 134 | 100.0 | 1102 | 91 | U49950 |
| 6 | 134 | 100.0 | 1164 | 10 | E15652 |
| 7 | 134 | 100.0 | 1164 | 10 | E17138 |
| 8 | 134 | 100.0 | 2894 | 10 | E15653 |

E15643: Human mRNA
E17135: Human mRNA
HS090434: Human mRNA
A0039046: Human mRNA
U49950: Human mRNA
E15652: Human gene
E17138: Human gene
E15653: Human gene

[illegible]

us-09-479-862-4.rng

Thu Aug 2 10:26:52 2001

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2001, 06:07:55 : Search time 4798.44 seconds
(without alignments)
434.475 Million cell updates/sec

Title: 08-09-479-862-4
Perfect score: 134
Sequence: 1 ATAAAGCAGCCGACGATA.....ACAAAATATTCTTTTAAG 134

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 10228115 seqs, 479426750 residues
Total number of hits satisfying chosen parameters: 20456210

Minimum OR seq length: 0
Maximum OR seq length: 2000000000
Post-processing: Minimum Match: 98
Listing first 45 summaries

Database : EST:
1: qb_est1:
2: qb_est2:
3: qb_est3:
4: qb_est4:
5: qb_est5:
6: qb_est6:
7: qb_est7:
8: qb_est8:
9: qb_est9:
10: qb_est10:
11: qb_est11:
12: qb_est12:
13: qb_est13:
14: qb_est14:
15: qb_est15:
16: qb_est16:
17: qb_est17:
18: qb_est18:
19: qb_est19:
20: qb_est20:
21: qb_est21:
22: qb_est22:
23: qb_est23:
24: qb_est24:
25: qb_est31:
26: qb_est34:
27: qb_est35:
28: qb_est36:
29: qb_est37:
30: qb_est38:
31: qb_est39:
32: qb_est40:
33: em_estba:
34: em_estfun:
35: em_esthum1:
36: em_esthum2:
37: em_esthum3:
38: em_esthum4:
39: em_esthum5:
40: em_esthum6:
41: em_esthum7:
42: em_esthum8:
43: em_esthum9:

44: em_esthum10:
45: em_esthum11:
46: em_esthum12:
47: em_esthum13:
48: em_esthum14:
49: em_esthum15:
50: em_esthum16:
51: em_esthum17:
52: em_esthum18:
53: em_esthum19:
54: em_esthum20:
55: em_esthum21:
56: em_esthum22:
57: em_esthum23:
58: em_esthum24:
59: em_esthum25:
60: em_esthum26:
61: em_esthum27:
62: em_esthum28:
63: em_estin1:
64: em_estin2:
65: em_estin3:
66: em_estin4:
67: em_estin5:
68: em_estin1:
69: em_estin2:
70: em_estov1:
71: em_estov2:
72: em_estpl1:
73: em_estpl2:
74: em_estpl3:
75: em_estpl4:
76: em_estpl5:
77: em_estpl6:
78: em_estpl7:
79: em_estpl8:
80: em_estpl9:
81: em_estpl10:
82: em_estrol:
83: em_estrol2:
84: em_estrol3:
85: em_estrol4:
86: em_estrol5:
87: em_estrol6:
88: em_estrol7:
89: em_estrol8:
90: em_estrol9:
91: em_estrol10:
92: em_estrol11:
93: em_estrol12:
94: em_estrol13:
95: em_estrol14:
96: em_estrol15:
97: em_estrol16:
98: em_estrol17:
99: em_estrol18:
100: em_estrol19:
101: em_estrol20:
102: qb_est25:
103: qb_est26:
104: qb_est27:
105: qb_est28:
106: qb_est29:
107: qb_est30:
108: qb_est31:
109: qb_est32:
110: qb_est41:
111: qb_est42:
112: qb_est43:
113: qb_est44:
114: qb_est45:
115: qb_est46:
116: qb_est47:

```

117: qb_est10: *
118: qb_est11: *
119: qb_est12: *
120: qb_est13: *
121: qb_est14: *
122: qb_est15: *
123: qb_est16: *
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125: qb_est18: *
126: qb_est19: *
127: qb_est20: *
128: qb_est21: *
129: qb_est22: *
130: qb_est23: *
131: qb_est24: *
132: qb_est25: *
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138: qb_est31: *
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170: qb_est63: *
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172: qb_est65: *
173: qb_est66: *
174: qb_est67: *
175: qb_est68: *
176: qb_est69: *
177: qb_est70: *
178: qb_est71: *
179: qb_est72: *
180: qb_est73: *
181: qb_est74: *
182: qb_est75: *
183: qb_est76: *
184: qb_est77: *
185: qb_est78: *
186: qb_est79: *
187: qb_est80: *
188: qb_est81: *
189: qb_est82: *

```

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being predicted
 and is derived by analysis of the total score distribution.

Thu Aug 2 10:26:59 2001

us-09-479-862-6.rni

```

1 IDENTIFICATION MESSAGE: S
US-08-884-424-6

Query Match
Best Local Similarity 100.0% Score 12: 108-43 Length 19:
Matches 12: Conservat 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGAG 12
1111111111
10 1 CUGAAGATGAG 12

RESULT 2
US-08-881-784-48
Sequence 48, Application US/08841784
GENERAL INFORMATION:
APPLICANT: Crotona, Rodney B.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE REFERENCE: WSO11463
CURRENT FILING DATE: 1999-04-14
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 49
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Patent 4,111,111
NAME/KEY: misc feature
LOCATION: (1)-(19)
OTHER INFORMATION: sequencing method
US-09-292-768-49

Query Match
Best Local Similarity 100.0% Score 12: 108-43 Length 19:
Matches 12: Conservat 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGAG 12
1111111111
10 1 CUGAAGATGAG 12

RESULT 4
Sequence 48, Application US/08199510
GENERAL INFORMATION:
APPLICANT: Bafarov, Carol
TITLE OF INVENTION: Anticommunotides With Anti-Epstein
TITLE OF INVENTION: Bar Virus Activity
NUMBER OF SEQUENCES: 3
CORRESPONDENT ADDRESS:
ADDRESS: 1400 N. Kosmos
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-479-862-6
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DECKET NUMBER: WSO119777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 224-0718
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1-19
OTHER INFORMATION: /product "Sequencing primer S17-1P2"
OTHER INFORMATION: (Table 2)
US-08-881-784-48

Query Match
Best Local Similarity 100.0% Score 12: 108-43 Length 19:
Matches 12: Conservat 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGAG 12
1111111111
10 1 CUGAAGATGAG 7

RESULT 5

```

TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-09-479-862-6

Query Match 100.0% Score 12: 100.0% Length 207
Best Local Similarity 100.0% Pred. No. 20-02
Matches 12: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGATG 12
DB 12 CUGAAGATGATG 1

RESULT 5
US-09-479-862-6 2/6
Sequence 2: Application US/09-281422
Patent No. 687854

GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-
BARR VIRUS ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA: US/09-281422
FILING DATE:
CLASSIFICATION: 514
ALTERNATIVE/AGENT INFORMATION:
NAME: Fasso, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE NUMBER: 1,270,413
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-09-479-862-6

Query Match 100.0% Score 12: 100.0% Length 207
Best Local Similarity 100.0% Pred. No. 20-02
Matches 12: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGATG 12
DB 12 CUGAAGATGATG 1

RESULT 6
US-09-479-862-6 2/6
Sequence 2: Application US/09-281422

GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-
BARR VIRUS ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lippitt & Kosmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/09-281422
FILING DATE:
CLASSIFICATION:
ALTERNATIVE/AGENT INFORMATION:
NAME: Kornek, Ann-Louise
REGISTRATION NUMBER: 33,524
REFERENCE NUMBER: 1,270,413
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-430-1400
TELEFAX: 617-430-1411
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-09-479-862-6

Query Match 100.0% Score 12: 100.0% Length 207
Best Local Similarity 100.0% Pred. No. 20-02
Matches 12: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGATG 12
DB 12 CUGAAGATGATG 1

RESULT 7
US-09-479-862-6 2/6
Sequence 2: Application US/09-281422

GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-
BARR VIRUS ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lippitt & Kosmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/09-281422
FILING DATE:

us-09-479-862-6.rni

Thu Aug 2 10:26:59 2001

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kethner, Ann Louise
REGISTRATION NUMBER: 43,924
REFERENCE/AGENT REFERENCE: NYZ 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-430-1400
TELEFAX: 617-430-1411
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08 199 510-1

Query Match
Best Local Similarity 100.0% Score 12: 106 2: Length 25:
Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CCGAGAGGATG 12
DB 20 CCGAGAGGATG 9

RESULT 8
US-08 628 422-1/3
Sequence 1: Application US/08028422
Patent No. 5847854
GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-POSSIBLE-POSS
TITLE OF INVENTION: VIRUS ACTIVITY
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08028422
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fasso, J. Peter
REGISTRATION NUMBER: 42,984
REFERENCE/AGENT REFERENCE: NYZ 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08 628-422-1

Query Match
Best Local Similarity 100.0% Score 12: 106 2: Length 25:
Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CCGAGAGGATG 12
DB 20 CCGAGAGGATG 9

RESULT 10
US-08 628 422-1/2
Sequence 1: Application US/08028422
Patent No. 5847854
GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-POSSIBLE-POSS
TITLE OF INVENTION: VIRUS ACTIVITY
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
US-08 628-422-1/2

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1  COUNTRY: USA
2  ZIP: 02109
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: Floppy disk
5  COMPUTER: IBM PC compatible
6  OPERATING SYSTEM: PC DOS/MS DOS
7  SOFTWARE: Patent in Release #1.0, Version #1.25
8  CURRENT APPLICATION DATA:
9  APPLICATION NUMBER: 1252895/02092
10 FILING DATE:
11 CLASSIFICATION:
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Forster, A.C. Esq.
14 REGISTRATION NUMBER: 33,523
15 REFERENCE/DOCKET NUMBER: HYZ-017991
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 617-330-1400
18 TELEFAX: 617-330-1211
19 INFORMATION FOR SEQ ID NO: 1:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 25 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: cDNA
26 HYPOTHETICAL: NO
27 ANTI-SENSE: YES
28 PRT US95-02082-1

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Query Match 100.0% Score 12; DB 5; Length 25;
Best local similarity 100.0% Pct. Id. 20-02;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;

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QY 1 CTGAAGATGAIG 12
DB 20 CTGAAGATGAIG 9

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RESULT 11
US-08-799-464A-12
1 Sequence 12, Application 05/08/95/09474A
2 Patent No. 5998601
3 GENERAL INFORMATION:
4 APPLICANT: Martandh, Michael P. et al.
5 TITLE OF INVENTION: VR 2342 VIRAL NUCLEOTIDE SEQUENCE AND
6 METHOD OF INVENTION: METHODS OF USE
7 NUMBER OF SEQUENCES: 25
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: John M. Collins
10 STREET: 2405 Grand Blvd., Suite 400
11 CITY: Kansas City
12 STATE: Missouri
13 COUNTRY: USA
14 ZIP: 64108
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC DOS/MS DOS
19 SOFTWARE: Patent in Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: 05/08/799-464A
22 FILING DATE:
23 CLASSIFICATION:
24 PRIOR APPLICATION: 546
25 APPLICATION NUMBER: 08/247,543
26 FILING DATE: August 5, 1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Collins, John M.
29 REGISTRATION NUMBER: 26,292
30 REFERENCE/DOCKET NUMBER: 22407
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (816) 474-9050

```

```

1 TELEFAX: (816) 474-9057
2 INFORMATION FOR SEQ ID NO: 12:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 369 base pairs
5 TYPE: nucleic acid
6 CHARGEDNESS: double
7 TOPOLOGY: linear
8 MOLECULE TYPE: cDNA
9 FEATURES:
10 NAME/KEY: CDS
11 LOCATION: 1..369
12 IDENTIFICATION METHOD: experimental
13 OTHER INFORMATION: /Evidence EXPERIMENTAL
14 OTHER INFORMATION: /Standard_name "VR 2342 REF 7"
15 US 08-799-464A-12

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Best local similarity 100.0% Pct. Id. 2.7e-02;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;

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QY 1 CTGAAGATGAIG 12
DB 176 CTGAAGATGAIG 187

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```

RESULT 12
PRT US95-09927-12
1 Sequence 12, Application 05/20/95/09927
2 GENERAL INFORMATION:
3 APPLICANT: Martandh, Michael P.
4 TITLE OF INVENTION: VR 2342 VIRAL NUCLEOTIDE SEQUENCE AND
5 METHOD OF INVENTION: METHODS OF USE
6 NUMBER OF SEQUENCES: 26
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: John M. Collins
9 STREET: 1101 Walnut, Suite 1400
10 CITY: Kansas City
11 STATE: Missouri
12 COUNTRY: USA
13 ZIP: 64106
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC DOS/MS-DOS
18 SOFTWARE: Patent in Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: PRT/05/09927
21 FILING DATE:
22 CLASSIFICATION:
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Collins, John M.
25 REGISTRATION NUMBER: 26122
26 REFERENCE/DOCKET NUMBER: 22987
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (816) 474-9050
29 TELEFAX: (816) 474-9057
30 INFORMATION FOR SEQ ID NO: 12:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 369 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: double
35 TOPOLOGY: linear
36 MOLECULE TYPE: cDNA
37 FEATURES:
38 NAME/KEY: CDS
39 LOCATION: 1..369
40 IDENTIFICATION METHOD: experimental
41 OTHER INFORMATION: /Evidence EXPERIMENTAL
42 OTHER INFORMATION: /Standard_name "VR 2342 REF 7"
43 PRT US95-09927-12

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us-09-479-862-6.rni

Thu Aug 2 10:26:59 2001

Query Match: 100.0%; Score 12; 100.0%; Length 469;
 Best Local Similarity: 100.0%; Pred. No. 2,700.02;
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;

07 1 CUGAAGATGATG 12
 14 176 CUGAAGATGATG 187

RESULT 14
 US 08-141-625B-16
 : Sequence 16, Application US/08/141625B
 : Patent No. 5695766

GENERAL INFORMATION:

APPLICANT: PAUL, PREM S.

APPLICANT: BALHUR, PATRICK C.

APPLICANT: MENG, XIANG JIN

APPLICANT: LDM, MELISSA A.

APPLICANT: LYOO, YOUNG S.

TITLE OF INVENTION: VACCINES AGAINST VIRUSES CAUSING PERSISTENT RESPIRATORY AND

TITLE OF INVENTION: REPRODUCTION OF PROTECTING A PIG AGAINST

TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: ORION, SIVAK, MCCELLAND, RATER & HERRLEID,

ADDRESSEE: P.C.

STREET: 1795 S. JEFFERSON DAVIS HIGHWAY, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compat file

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/141625B

FILING DATE: 05 OCT-1994

CLASSIFICATION: 4.45

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/969,071

FILING DATE: 08 OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lavalleye, Jean-Paul M.P.

REGISTRATION NUMBER: 31,451

REFERENCE/AGENT NUMBER: 4,25 014 55X CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-4000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 472 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: porcine reproductive and respiratory syndrome

STRAIN: Iowa

INDIVIDUAL ISOLATE: ISD-12

FEATURE:

NAME/KEY: CDS

LOCAL ID: 1-469

US 08-141-625B-16

Query Match: 100.0%; Score 12; 100.0%; Length 472;
 Best Local Similarity: 100.0%; Pred. No. 2,700.02;
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;

07 1 CUGAAGATGATG 12
 14 176 CUGAAGATGATG 187

RESULT 14
 US 08-855-541D-14
 : Sequence 14, Application US/08/855541D
 : Patent No. 6110467

GENERAL INFORMATION:

APPLICANT: PREM, PAUL S.

APPLICANT: BALHUR, PATRICK C.

APPLICANT: MENG, XIANG JIN

APPLICANT: LDM, MELISSA A.

APPLICANT: LYOO, YOUNG S.

TITLE OF INVENTION: VACCINES AGAINST VIRUSES CAUSING PERSISTENT RESPIRATORY AND

TITLE OF INVENTION: REPRODUCTION OF PROTECTING A PIG AGAINST

TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: ORION, SIVAK, MCCELLAND, RATER & HERRLEID,

ADDRESSEE: P.C.

STREET: 1795 S. JEFFERSON DAVIS HIGHWAY, Suite 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compat file

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/2805541D

FILING DATE: 13 May-1997

CLASSIFICATION: unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/969,071

FILING DATE: 08 OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: LAVALLEYE, JEAN PAUL M.P.

REGISTRATION NUMBER: 31,451

REFERENCE/AGENT NUMBER: 4,25 014 55X CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703 413-4000

TELEFAX: 703 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 472 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Porcine reproductive and respiratory syndrome

STRAIN: Iowa

INDIVIDUAL ISOLATE: ISD-12

SEQUENCE DESCRIPTION: SEQ ID NO: 14;

US 08-855-541D-14

Query Match: 100.0%; Score 12; 100.0%; Length 472;
 Best Local Similarity: 100.0%; Pred. No. 2,700.02;
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;

07 1 CUGAAGATGATG 12
 14 176 CUGAAGATGATG 187

RESULT 15

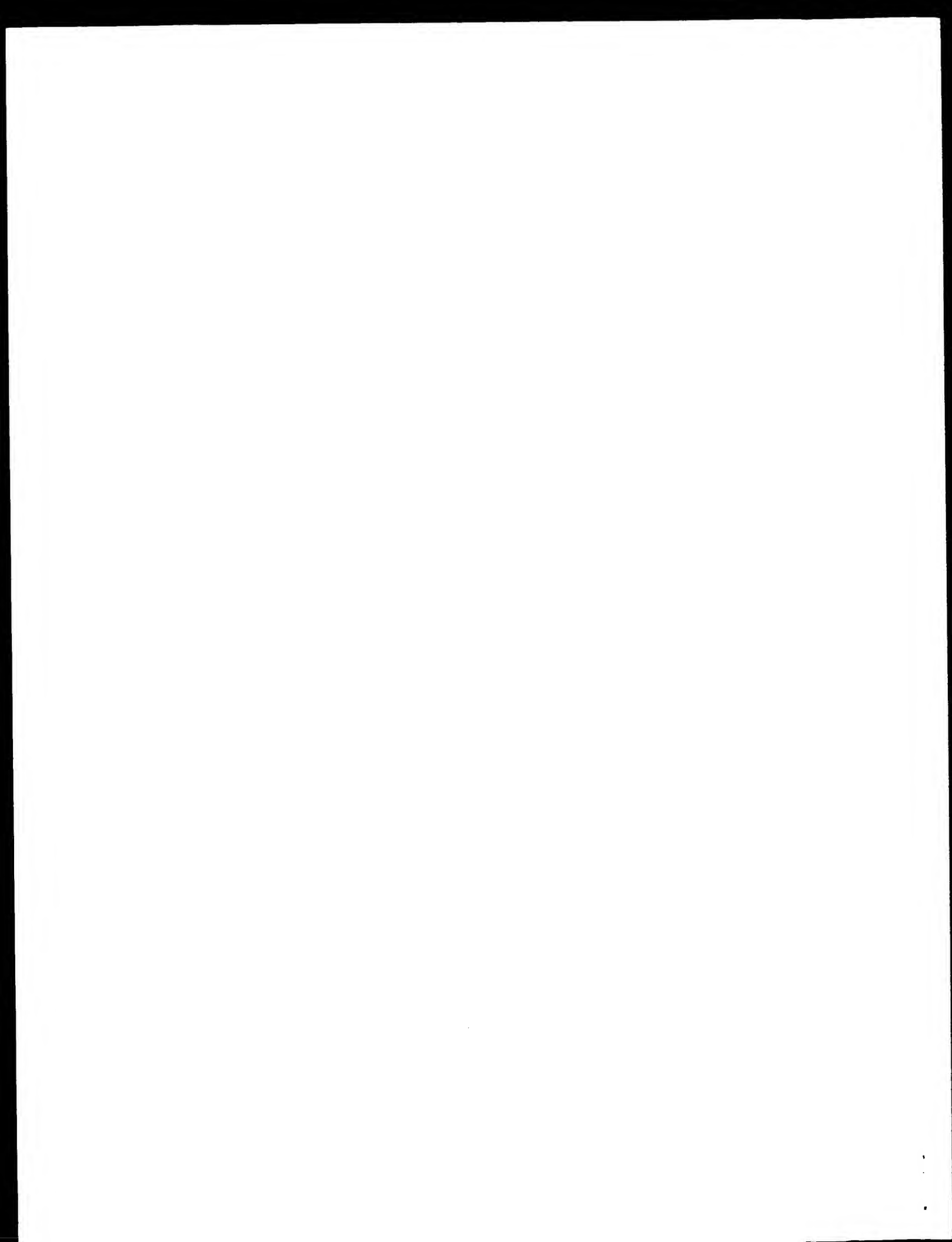
US-09-855-526B-14
 : Sequence 14: Application US/0855526B
 : Patent No. 6,251,404
 : GENERAL INFORMATION:
 : APPLICANT: DEEM, PAUL S.
 : APPLICANT: BALBOA, DAVID G.
 : APPLICANT: KING, XIANG JIN
 : APPLICANT: LOM, MELISSA A.
 : APPLICANT: LYON, YOUNG S.
 : TITLE OF INVENTION: VACCINES AGAINST AN EBOLA-LIKE VIRUS
 : TITLE OF INVENTION: RESPONSE AGAINST VIRUSES CAUSING FEVER, RESPIRATORY AND
 : TITLE OF INVENTION: REPRODUCTIVE DISEASES, METHODS OF PREVENTING A DISEASE
 : TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
 : NUMBER OF SEQUENCES: 47
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: OBLON, SPIVAK, MUELLER, MATER & NEUBAUER
 : ADDRESSEE: P.C.
 : STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 : CITY: ARLINGTON
 : STATE: VA
 : COUNTRY: USA
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC DOS/MS DOS
 : SOFTWARE: Patent to Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: 09/0855526B
 : FILING DATE: 13-MAY-1997
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/969,071
 : FILING DATE: 30-OCT-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: LAVALLEY, JEAN-PAUL M.P.
 : REGISTRATION NUMBER: 41,451
 : REFERENCE/PACKET NUMBER: 4425-040 55X 51V
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 703-413-4000
 : TELEFAX: 703-413-2220
 : TELEX: 248955 GFAT DR
 : INFORMATION FOR SEQ ID NO: 14:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 372 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: unknown
 : TOPOLOGY: unknown
 : MOLECULE TYPE: cDNA
 : ORIGINAL SOURCE:
 : ORGANISM: Porcine reproductive and respiratory syndrome
 : ORGANISM: Virus
 : STRAIN: Iowa
 : INDIVIDUAL ISOLATE: IS0 12
 : US 09 855-526B-14

Query Match 100.0% Score 127 Sub 4; Length 372
 Best Local Similarity 100.0% Pct. No. 2, 70-000
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 1 CTGAGATGATG 12

Db 176 CTGAGATGATG 187

Search completed: August 2, 2001, 07:12:41
 Job time: 7847 sec



Genfore version 1.5
Copyright (c) 1993 - 2000 Computer U.S.A.

OM nucleic nucleic search, using sw model

Run on: August 2, 2001, 07:17:45, March time 202.02 seconds
(without alignments)
25.723 H:1.56, 3.11 up 14.03, 5.0

Title: US-09-479-862-4
Perfect score: 12
Sequence: 1 CTGAAGATGATC 12

Scoring table: IDENTITY_NMC
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 314950809 residues

Total number of hits satisfying chosen parameters: 1469292

Minimum DB seq length: 0
Maximum FP seq length: 200000000

Post processing: Minimum Match 60
Maximum Match 100%
Listing first 45 summaries

| Database : | N_Geneseq_0601:* |
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| 3: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
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| 6: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
| 7: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
| 8: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
| 9: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
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| 12: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
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| 19: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
| 20: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
| 21: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |
| 22: | US-09-479-862-4 (human) (Geneseq) NA1985-1A1 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| C 1 | 12 | 100.0 | 19 | 20 | AA06592 |
| C 2 | 12 | 100.0 | 19 | 22 | AA07609 |
| C 3 | 12 | 100.0 | 20 | 14 | AA041581 |
| C 4 | 12 | 100.0 | 20 | 16 | AA001769 |
| C 5 | 12 | 100.0 | 20 | 18 | AA092691 |
| C 6 | 12 | 100.0 | 20 | 19 | AA028262 |
| C 7 | 12 | 100.0 | 20 | 20 | AA023647 |
| C 8 | 12 | 100.0 | 20 | 20 | AA018784 |
| C 9 | 12 | 100.0 | 20 | 21 | AA049377 |
| C 10 | 12 | 100.0 | 25 | 16 | AA033757 |
| C 11 | 12 | 100.0 | 25 | 18 | AA092594 |

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|------|----|-------|-----|----|----------|
| C 12 | 12 | 100.0 | 25 | 18 | AA092690 |
| C 13 | 12 | 100.0 | 25 | 19 | AA028261 |
| C 14 | 12 | 100.0 | 25 | 20 | AA024662 |
| C 15 | 12 | 100.0 | 25 | 20 | AA018783 |
| C 16 | 12 | 100.0 | 25 | 21 | AA049376 |
| C 17 | 12 | 100.0 | 54 | 22 | AA062199 |
| C 18 | 12 | 100.0 | 75 | 22 | AA062197 |
| C 19 | 12 | 100.0 | 95 | 22 | AA027011 |
| C 20 | 12 | 100.0 | 131 | 21 | AA069812 |
| C 21 | 12 | 100.0 | 133 | 21 | AA024316 |
| C 22 | 12 | 100.0 | 144 | 21 | AA030712 |
| C 23 | 12 | 100.0 | 235 | 16 | AA025236 |
| C 24 | 12 | 100.0 | 238 | 21 | AA093581 |
| C 25 | 12 | 100.0 | 240 | 20 | AA055756 |
| C 26 | 12 | 100.0 | 242 | 21 | AA012628 |
| C 27 | 12 | 100.0 | 259 | 20 | AA069975 |
| C 28 | 12 | 100.0 | 274 | 21 | AA014874 |
| C 29 | 12 | 100.0 | 286 | 21 | AA087100 |
| C 30 | 12 | 100.0 | 300 | 20 | AA012905 |
| C 31 | 12 | 100.0 | 300 | 20 | AA012905 |
| C 32 | 12 | 100.0 | 300 | 20 | AA012905 |
| C 33 | 12 | 100.0 | 300 | 21 | AA012338 |
| C 34 | 12 | 100.0 | 335 | 21 | AA007023 |
| C 35 | 12 | 100.0 | 342 | 20 | AA090244 |
| C 36 | 12 | 100.0 | 344 | 21 | AA021958 |
| C 37 | 12 | 100.0 | 369 | 17 | AA016245 |
| C 38 | 12 | 100.0 | 370 | 20 | AA089660 |
| C 39 | 12 | 100.0 | 372 | 18 | AA063596 |
| C 40 | 12 | 100.0 | 372 | 17 | AA013392 |
| C 41 | 12 | 100.0 | 372 | 17 | AA014416 |
| C 42 | 12 | 100.0 | 372 | 17 | AA014417 |
| C 43 | 12 | 100.0 | 372 | 17 | AA014418 |
| C 44 | 12 | 100.0 | 372 | 17 | AA014419 |
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ALIGNMENTS

RESULT 1

AA014420 (1) 100.0 standard: DNA; 19 BP.

AA014420 (2) 100.0

AA014420 (3) 100.0

AA014420 (4) 100.0

AA014420 (5) 100.0

AA014420 (6) 100.0

AA014420 (7) 100.0

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AA014420 (9) 100.0

AA014420 (10) 100.0

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AA014420 (20) 100.0

AA014420 (21) 100.0

AA014420 (22) 100.0

AA014420 (23) 100.0

AA014420 (24) 100.0

PI to produce trans carved and trans isopiperitenol
 XX
 XX Example 5; Page 41; 80pp; English.
 XX
 CC The invention relates to nucleotide sequences encoding spearmint
 CC (-) limonene-6-hydroxylase (L6H) and peppermint (-) limonene-8-
 CC hydroxylase (L8H). Host cells containing a vector comprising the
 CC nucleotide sequences can be used for the recombinant production of
 CC limonene hydroxylases or as primary enzyme products. The primary enzyme
 CC products are trans-carved in the case of (-)-L6H or
 CC trans isopiperitenol in the case of (-)-L8H, which are of subsequent use,
 CC to obtain enhanced expression of limonene hydroxylase in plants to attain
 CC enhanced trans carved or trans-isopiperitenol production as a predator
 CC or pathogen defense mechanism, attractant or environmental signal. The
 CC limonene hydroxylase cDNAs also provide a useful tool for isolating
 CC other monoterpene hydroxylase genes and cDNAs from other plants.
 CC regulation of monoterpene biosynthesis. Sequences AAX06574-604 represent
 CC (-)-limonene-6-hydroxylase cDNA sequences. Plasmids which were also
 CC used to construct the cDNA hybridisation probe III 2 (AAX06562).
 XX
 SQ Sequence 19 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 12; 10 20; Length 19;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; gaps 0;
 QY 1 CCGAAGATGATG 12
 DB 18 CCGAAGATGATG 7

RESULT 2
 AAF76648Z
 ID AAF76648 standard; DNA; 19 BP;
 XX
 AC AAF76648;
 XX
 XX 15 MAY 2001 (first entry)
 XX
 DE Spearmint limonene hydroxylase; PEP plant; SEQ ID NO: 19;
 XX
 XX Spearmint; peppermint; (-)-limonene-6-hydroxylase;
 KW (-)-limonene-3-hydroxylase; limonene; aroma; plant; PEP plant; see
 XX
 XX Mentha spicata.
 CS
 XX 056194185 RI.
 XX
 XX 27-FEB-2001.
 XX
 XX 14-APR-1999; 9908-0292768.
 XX
 XX 24-JUN-1997; 9705-0881784.
 XX
 XX (UNIW) UNIV WASHINGTON STATE RIS FOUND.
 XX
 XX Crotona RB; Lupton SL; Karp F;
 XX
 XX WP1; 2001 243405/25.
 XX
 XX R 011 15-01-03 436 mg by hydroxylase. The 15-01-03 436 mg by
 PI useful for after production of limonene-6-hydroxylase or
 PI limonene-3-hydroxylase in suitable host cell
 XX

Example 5; Column 63; 57pp; English.
 XX
 CC the present invention provides the proteins and cDNAs prepared of the
 CC peppermint and spearmint (-) limonene-3-hydroxylase and the spearmint
 CC (-) limonene-6-hydroxylase. Also provided are a number of primers and PCR
 CC primers which were used to isolate the sequences. These are useful in the
 CC production of transgenic plants with altered flavor and aroma.
 XX

SQ Sequence 19 BP; 5 A; 7 C; 4 G; 4 T; 0 other;
 Query Match
 Best Local Similarity 100.0%; Score 12; 10 20; Length 19;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; gaps 0;
 QY 1 CCGAAGATGATG 12
 DB 18 CCGAAGATGATG 7

K23833 3
 AA041541Z
 ID AA041541 standard; DNA; 20 BP;
 XX
 AC AA041541;
 XX
 XX 10-AUG-1994 (first entry)
 XX
 DE Antisense oligomer targeting ZLF 1 AUG site.
 XX
 KW Epstein Barr virus; EBV; hybridisation; and license modulation;
 KW replication; nasopharyngeal carcinoma; Burkitt lymphoma; Epstein Barr
 XX syndrome; infectious mononucleosis; latent; active; infected; 38
 CS Synthetic;
 XX
 XX W0930/882 A;
 XX
 XX 29 APR 1994;
 XX
 XX 24 OCT 1992; 92WO 0508989;
 XX
 XX 25 OCT 1991; 91US 0784605;
 XX
 XX (ISIS) ISIS PHARM INC;
 XX
 XX Anderson KP; Ecker DJ;
 XX
 XX W11 1993 1211718;
 XX
 XX Ethanol nucleotide (s) hybridising with RNA of Epstein Barr virus
 PI for treating a live, latent and chronic EBV infections and
 PI associated diseases e.g. nasopharyngeal carcinoma, Burkitt's
 PI lymphoma
 XX
 PS Claim 1; Page 20; 45pp; English.
 CC The synthetic peptide is an antisense modulator of Epstein Barr
 CC virus and protein, contains at least one phosphothioate linking of
 CC and modifications in the 2' position. These modifications improve
 CC penetration into regions of the cell that contain nucleic acid and
 CC also resistance to degradation by nucleases. The oligonucleotide
 CC targets the AUG site of ZLF-1 and hybridises, thus
 CC inhibiting or preventing EBV-associated diseases, e.g. nasopharyngeal
 CC carcinoma, Burkitt's lymphoma, Sjogren's syndrome, infectious
 CC mononucleosis etc. The oligomer is effective against both latent and
 CC active EBV infection.
 CC See also AA040575 9 and AA041517 44.
 XX
 SQ Sequence 20 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 12; 10 14; Length 20;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; gaps 0;
 QY 1 CCGAAGATGATG 12
 DB 15 CCGAAGATGATG 4

Thu Aug 2 10:26:58 2001

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PR 19 DEC-1996; 96US-0769951.
XX (ISIS-) ISIS PHARM INC.
PA Chen D, Cole DL, Srivatsa GS;
XX WFL 1998 429242/1.
XX Matrix for selective separation of oligonucleotide, useful for,
PR e.g., large scale purification of anti-sense agents from their
PI deletion derivatives formed during synthesis
XX disclosure, Page 152; 184pp; English.
XX AAV24195, 268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that
XX comprises a support and an affinity unit that specifically and
XX reversibly binds a target oligonucleotide, and comprises a sequence of
XX bases having the reverse complement of a hybridising portion of the
XX target oligonucleotide. The matrix is used for affinity purification of
XX synthetic oligonucleotides, specifically antisense agents, for treatment
XX of hyperproliferative diseases, e.g., Alzheimer's, for modulating
XX expression of cell surface proteins, and to inhibit a eukaryotic
XX pathogen, retrovirus or other viruses.
XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;
SQ

Query Match 100.0%; Score 12; BB 19; Length 20;
Best Local Similarity 100.0%; Prod. No. 7,96,002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGAATGATG 12
BB 12 CTGAAGAATGATG 1

RESULT 7
AAAX23663A
ID AAX24663 standard; DNA; 20 BP.
XX AAX24663;
AC AAX24663;
XX 18-JUN-1999 (first entry)
XX deletion sequence oligonucleotide 116.
XX deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; SS.
XX Synthetic.
XX W09011820 A1.
XX 11-MAR-1999.
XX 01-SEP-1998; 98WO-US18084.
XX 02-SEP-1997; 97US-0924771.
XX (ISIS-) ISIS PHARM INC.
XX Chen D, Srivatsa GS;
XX WFL 1999-205198/17.
XX New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides

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PS Example 7; Page 108; 164pp; English.
XX This invention describes a novel composition comprising a random
XX sensor array, where each array comprises a unique probe
XX oligonucleotide, which is the reverse complement of part of a unique
XX target oligonucleotide present in a mixture of target deletion
XX oligonucleotides. The compositions form a method for characterizing a
XX sample of target deletion oligonucleotides which are labelled and
XX hybridize with the probe oligonucleotides of the sensor array.
XX oligonucleotides and their targets are represented in AAX, 04p 26-30.
XX oligonucleotides characterized by the method form pharmaceutical
XX compositions that are useful for modulating cellular adhesion,
XX proliferation, and being active against a eukaryotic pathogen, a human
XX retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX retrovirus, including influenza virus, Epstein Barr virus, hepatitis
XX Syncytial virus or cytomegalovirus (CMV). The compositions enable
XX characterization of deletion sequences, and quantification of different
XX but different nucleobase sequences, and quantification of different
XX species of deletion sequence ("target") oligonucleotides in a mixture.
XX Also, if the specificity of the oligonucleotide's nucleobase sequence
XX for its reverse complement is not modified, the method may be performed
XX using oligodeoxynucleotides.
XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;
SQ

Query Match 100.0%; Score 12; BB 20; Length 20;
Best Local Similarity 100.0%; Prod. No. 7,96,002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGAATGATG 12
BB 12 CTGAAGAATGATG 1

RESULT 8
AAAX18784C
ID AAX18784 standard; DNA; 20 BP.
XX AAX18784;
AC AAX18784;
XX 10 MAY 1999 (first entry)
XX Target Epstein Barr virus and isuse of oligonucleotide #116.
XX Cellular adhesion protein; proliferation; and isuse of oligonucleotide
XX affinity canal; transport; gastrointestinal mucosa; cancer;
XX Alzheimer's disease; beta thalassemia; malaria; viral infection;
XX HIV; inflammation; SS.
XX Synthetic.
XX W0901579 A1.
XX 14-JAN-1999.
XX 01-JUL-1998; 98WO-US13574.
XX 01-JUL-1997; 97US-0886829.
XX (ISIS-) ISIS PHARM INC.
XX Barbee G, Tetat C;
XX WFL 1999 106077/09.
XX Composition comprising nucleic acid and penetration enhancer, used
XX particularly for delivering therapeutic and isuse of oligonucleotide
XX across the gastrointestinal mucosa, provides high bioavailability.
XX Example 2; Page 108; 115pp; English.
XX A pharmaceutical composition has been developed which comprises
XX

```


CC nucleic acid and at least one penetrant to enhance the compositions are
 CC used; (i) to treat a prevent any disease of the digestive tract
 CC treated with the nucleic acid; (ii) to prevent any disease of the digestive tract
 CC beta-thalassemia, malaria, viral infections (including human immune
 CC deficiency virus (HIV)), inflammation, to human or animal models;
 CC (ii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-45%, the penetration enhance improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AAX18669 to AAX18799 and AAX18801
 CC represent antisense oligonucleotides which can be used as the nucleic
 CC acid in the method of the invention.

XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;

Query Match 100.0%; Score 12; PB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e-02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAAGATG 12

1111111111

12 CTGAAGATG 1

RESULT 9

AA24377A

ID AA24377 standard; DNA: 20 BP

XX AA24377;

XX AA24377;

14 MAR 2000 (first entry)

XX Epstein Barr virus targeted antisense oligonucleotide (EBV) in 42.

XX Viral infection; expression; modulation; antisense;

XX non-parenteral delivery; antisense oligonucleotide; modulation;

XX ulcerative colitis; Crohn's disease; inflammatory bowel disease;

XX cellular proliferation; ss.

XX Synthetic.

XX Epstein-Barr virus.

XX W9960012-A1.

XX 25-MAY-1999; 9960-0811994.

XX 20-MAY-1999; 9960-0811994.

XX 21-MAY-1998; 9805-0082624.

XX (US15) 15TS PHARM INC

XX long C; Cook PB; Williams; Hargrove; Hargrove; Hargrove; Hargrove;

XX WPI: 2000-0729/905.

XX New oligonucleotide compositions used for the non-parenteral delivery

XX of anti-sense oligos, ribozymes, peptide nucleic acids, molecular

XX decoys, external guide sequences or aptamers

XX Example 2, Page 129, 139pp, English.

XX Sequences AA24377A 24377A, AA24377B and AA24377C represent antisense

XX oligonucleotides destined to have therapeutic activity against certain

XX non-retroviral viruses. The invention relates to new compositions for

XX the non-parenteral delivery of oligonucleotides comprising at

XX least one oligonucleotide in an emulsion, oligonucleotides

XX delivered via the compositions of the invention can be used to modulate

XX expression of a cellular adhesion protein, modulate a rate of cellular

CC proliferation, or have biological activity against cytokines, chemokines
 CC and interleukins. They can be used in treating conditions including
 CC or under cellular proliferation, Crohn's disease, inflammatory bowel disease,
 CC and osteoporosis and delivery of nucleic acid via non-parenteral
 CC routes of administration (e.g., via the alimentary canal, rectal, vagi,
 CC pulmonary tract, urethra or vagina).

XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 12; PB 21; Length 20;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAAGATG 12

1111111111

12 CTGAAGATG 1

RESULT 10

AA24377A

ID AA24377 standard; DNA: 25 BP

XX AA24377;

XX AA24377;

22 MAR 1996 (first entry)

XX Synthetic oligonucleotide #1 hybridisable to BZLF1 RNA.

XX BZLF1: Epstein Barr virus; EBV; therapy; ss.

XX Synthetic.

XX W9960012-A1.

XX 24 APR 1995.

XX 17 FEB 1995; 9960-0502082.

XX 18 FEB 1994; 9405-0199510.

XX (BYBR) HYBRIDON INC.

XX Mulder C;

XX WPI: 1995-02685/99.

XX oligonucleotide(s) having anti-Epstein Barr Virus activity in

XX complementary to a portion of the BZLF1 RNA of EBV

XX Claim 19; Page 41; 47pp; English.

XX The sequences represented by AA24377-59 are synthetic oligonucleotides

XX that are complementary to and hybridisable with a portion of the BZLF1

XX RNA of Epstein Barr Virus (EBV). BZLF1 is the first gene activated in

XX the life cycle of EBV. This sequence is complementary to 25

XX nucleotides of the region flanking the initiation codon. These sequences

XX hybridize to the region of mRNA immediately surrounding the translational

XX initiation codon and thereby prevent synthesis of BZLF1. These sequences

XX can be altered to contain modified interlinked linkages (e.g.,

XX triphosphates, phosphorothioate, carbamate, carbonate, phosphate,

XX triester, and others) without compromising their ability to hybridize

XX BZLF1 mRNA. The sequences can be used in pharmaceutical compositions

XX which inhibit the replication of EBV in a cell. The compositions can

XX therefore be used in treatment of EBV infection.

XX Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;

SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 12; PB 16; Length 25;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAAGATG 12

1111111111

12 CTGAAGATG 1

QY 1 CTGAAGATGAG 12
 1111111111
 20 CTGAAGATGAG 9

RESULT 11
 AAT92694
 ID AAT92694 standard; DNA; 25 BP.

XX AC AAT92694;
 XX 22-APR-1998 (first entry)

DE Sense sequence S25 of BZLF1 antisense oligonucleotide Z1.
 XX Epstein-Barr virus; antisense oligonucleotide; PBV; treatment: tumour;
 KW terminal protein; BZLF1, BRLF1, BRLF1; BRLF1; BRLF1;
 KW BZLF2; BSLF2; sense sequence; SS.

XX Synthetic.
 OS Epstein-Barr virus.
 XX W09747669 AL.
 XX 16-OCT-1997.

XX 04 APR 1997; 97W0-US06104.
 XX 05 APR 1996; 96US-0628422.
 XX (OYMA) UNIV MASSACHUSETTS.
 XX Muller C;

XX WP1; 1997 512405/47.
 XX Antisense oligonucleotide(s) that inhibit Epstein Barr virus
 PF function - used to treat or prevent EB virus infections, including
 PT tumours

XX Disclosure; Page 64; 79pp; English.
 XX This is the sense sequence of the antisense oligonucleotide Z1 specific
 CC to a portion of a BZLF1 gene. Antisense oligonucleotides specific to any
 CC of the different strains of Epstein Barr virus (EBV) such as the BZLF1,
 CC BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1,
 CC proteins 1 and 2 are used to inhibit EBV function. This S25 acts as a
 CC negative control in the synthesis of such antisense oligonucleotides. The
 CC antisense oligonucleotides are antisense sequences that inhibit EBV
 CC replication or gene expression. The antisense oligonucleotides or the
 CC vectors expressing them, are used to treat or prevent EBV infection
 CC (including tumours such as nasopharyngeal carcinoma) in mammals. When
 CC labelled, they can also be used to detect cells infected with EBV. The
 CC antisense oligonucleotides can be targeted to either the latent or the
 CC lytic phase of the virus cycle. Combinations of the antisense
 CC oligonucleotides directed against different viral genes may provide a
 CC synergistic inhibitory effect. Formulation of these antisense
 CC oligonucleotides with transfection agents can increase the efficiency
 CC and reduce their needed dosage.

XX Sequence 25 BP; 8 A; 5 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 12; DB 18; Length 25;
 Best local Similarity 100.0%; Prod. No. 81-0022
 Matches 12; Conservation 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGAG 12
 1111111111
 6 ctgaatgatg 17

RESULT 12
 AAT92694/C
 ID AAT92694 standard; DNA; 25 BP.

XX AC AAT92694;
 XX 22 APR 1998 (first entry)

DE BZLF1 gene specific antisense oligonucleotide Z1.
 XX Epstein Barr virus; antisense oligonucleotide; PBV; treatment: tumour;
 KW terminal protein; BZLF1, BRLF1, BRLF1; BRLF1; BRLF1;
 KW BZLF2; BSLF2; sense sequence; SS.

XX Synthetic.
 OS Epstein Barr virus.
 XX W09747669 AL.
 XX 16 OCT 1997.

XX 04 APR 1997; 97W0-US06104.
 XX 05 APR 1996; 96US-0628422.
 XX (OYMA) UNIV MASSACHUSETTS.
 XX Muller C;

XX WP1; 1997 512405/47.

XX Antisense oligonucleotide(s) that inhibit Epstein Barr virus.
 PF function - used to treat or prevent EB virus infections, including
 PT tumours

XX Disclosure; Page 64; 79pp; English.

XX This antisense oligonucleotide is specific to a portion of the BZLF1
 CC gene. Antisense oligonucleotides specific to any of the different
 CC strains of Epstein Barr virus (EBV) such as the BZLF1, BRLF1, BRLF1,
 CC BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1, BRLF1,
 CC proteins 1 and 2 are used to inhibit EBV function. These antisense oligonucleotides are
 CC antisense sequences that inhibit EBV replication or gene expression. The
 CC antisense oligonucleotides or the vectors expressing them, are used to
 CC treat or prevent EBV infection (including tumours such as nasopharyngeal
 CC carcinoma) in mammals. When labelled, they can also be used to detect
 CC cells infected with EBV. The antisense oligonucleotides can be targeted
 CC to either the latent or the lytic phase of the virus cycle. Combinations
 CC of the antisense oligonucleotides directed against different viral genes
 CC may provide a synergistic inhibitory effect. Formulation of these
 CC antisense oligonucleotides with transfection agents can increase the
 CC efficiency and reduce their needed dosage.

XX Sequence 25 BP; 8 A; 6 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 12; DB 18; Length 25;
 Best local Similarity 100.0%; Prod. No. 81-0022
 Matches 12; Conservation 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGAG 12
 1111111111
 20 ctgaatgatg 9

RESULT 14
 AAT92694/C
 ID AAT92694 standard; DNA; 25 BP.

XX AC AAT92694;
 XX 08 OCT 1998 (first entry)

DE Antisense oligonucleotide to cytomegalovirus.

XX purification: oligonucleotide matrix: primary anti-viral modulators;
 KW affinity purification: antisense: influenza virus; CMV; ss;
 XX Synthelec;
 XX Cytomegalovirus;
 XX W 9827425 Al;
 XX 25-JUN-1998;
 XX 18-DEC-1997; 97WS-US24284;
 XX 19-DEC-1996; 96US-0769951;
 XX (ISIS-) ISIS PHARM INC;
 XX Chen D, Cole D, Sargis J;
 XX WPL: 1998-362922/1;
 XX Matrix for selective separation of oligonucleotide - useful for;
 XX cdc, large scale purification of antisense agents from their;
 XX deletion derivatives formed during synthesis;
 XX disclosure; Page 151; 184pp; English;
 XX AAV28155-268 represent oligonucleotides which can be purified using the;
 XX method of the invention. The specification describes a matrix that;
 XX comprises a support and an affinity unit that specifically and;
 XX reversibly binds a target oligonucleotide, and comprises a sequence of;
 XX bases having the reverse complement of a hybridization portion of the;
 XX target oligonucleotide. The matrix is used for affinity purification of;
 XX synthetic oligonucleotides. The matrix is used for affinity purification of;
 XX hyperproliferative diseases, specifically antisense agents, for treatment;
 XX of hyperproliferative diseases, such as Alzheimer's, for modulation;
 XX expression of cell surface proteins, and to inhibit a eukaryotic;
 XX pathogen, retrovirus or other viruses;
 XX Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 12; DB 19; Length 25;
 Best Local Similarity 100.0%; Pred. No. 8,10-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGAAGATGATG 12
 |||||
 TB 20 CUGAAGATGATG 9
 RESULT 14
 AAX23662;
 ID AAX23662 standard; DNA; 25 BP;
 AC
 AAX23662;
 18-JUN-1999 (first entry)

XX deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
 KW probe; cellular adhesion modulator; cellular proliferation modulator;
 KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
 KW HIV; primer; ss
 XX Synthelec;
 XX W 9911820-Al;
 XX 11-MAR-1999;
 XX 01-SEP-1998; 98WS-US18084;

XX 02-SEP-1997; 97WS-0922771;
 XX (ISIS-) ISIS PHARM INC;
 XX Chen D, Sargis J;
 XX WPL: 1998-205148/17;
 XX New compositions comprising sensor arrays made up of unique probe;
 XX oligonucleotides - useful for characterizing a sample of target;
 XX deletion oligonucleotides
 XX Example 9; Page 188; 164pp; English;
 XX This invention describes a novel composition comprising a number of;
 XX sensor arrays, where each array comprises a unique probe;
 XX oligonucleotide, which is the reverse complement of part of a unique;
 XX target oligonucleotide present in a mixture of target deletion sequence;
 XX oligonucleotides. The compositions form a method for characterizing a;
 XX sample of target deletion oligonucleotides which are labeled and;
 XX hybridize with the probe oligonucleotides of the sensor arrays. The;
 XX oligonucleotides and their targets are represented in AAX23662-Al;
 XX oligonucleotides characterized by the method form pharmaceutical;
 XX compositions that are useful for modulating cellular adhesion, or;
 XX proliferation, and being active against a eukaryotic pathogen, a human;
 XX retrovirus, a human immunodeficiency virus (HIV), or a non-human;
 XX retrovirus, including influenza virus, Epstein-Barr virus, Respiratory;
 XX Syncytial Virus or cytomegalovirus (CMV). The compositions enable;
 XX characterization of deletion sequence oligonucleotides having related;
 XX but different nucleobase sequences, and quantification of different;
 XX species of deletion sequence ("target") oligonucleotides in a mixture;
 XX Also, if the specificity of the oligonucleotide's nucleobase sequence;
 XX for its reverse complement is not modified, the method may be performed;
 XX using oligo-deoxynucleotides;
 XX Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 8,10-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGAAGATGATG 12
 |||||
 TB 20 CUGAAGATGATG 9
 RESULT 15
 AAX18783;
 ID AAX18783 standard; DNA; 25 BP;
 AC
 AAX18783;
 10-MAY-1999 (first entry)

XX target: Epstein-Barr virus antisense oligonucleotide #115;
 KW cellular adhesion protein; proliferation; antisense oligonucleotide;
 KW alimentary canal; transport; gastrointestinal mucosa; cancer;
 KW Alzheimer's disease; tetra-thaumasia; malaria; viral infection;
 KW HIV; inflammation; ss;
 XX Synthelec;
 XX W 9901579-Al;
 XX 14-JAN-1999;
 XX 01-JUL-1998; 98WS-US13574;
 XX 01-JUL-1997; 97WS-0886829;
 XX

PA (ISIS-) ISIS PHARM INC.
XX
PI Bardee G. Teot C;
XX
DK WPI; 1999 106077/09.
XX
PI Composition comprising nucleic acid and penetration enhancer used
PI particularly for delivering therapeutic antisense oligonucleotides
PI across the gastrointestinal mucosa, provides high bioavailability
XX
PS Example 2; Page 108; 115pp; English.
XX
CC A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC used: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35%. The penetration enhancer improves: (i) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid. Oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAX16669 to AAX18799 and AAX18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 12; E-8 20; Length 25;
Best Local Similarity 100.0%; P-adj. No. 8; Rev 02;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;
0Y 1 CTCAGATGATG 12
06 11111111111
06 20 CTCAGATGATG 9

Search completed: August 2, 2001, 07:17:46
Job time: 804.2 sec

Genome version 4.5
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EM Estimator: nucleic search, using sw model

Run on: August 2, 2001 06:08:00 : Search time: 3700.43 seconds
(without alignments)
29,863 Million cell updates/sec

Title: us-09-479-862-6
Project source: 12
Sequence: 1 CCGAAGAGATG 12

Scoring table: IDENTITY_NUC
Gapop 10.0 : Gapext 1.0

Searches: 1022815 seqs, 4726429760 residues 20196260
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum EB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST: *
1: qb_est1: *
2: qb_est2: *
3: qb_est3: *
4: qb_est4: *
5: qb_est5: *
6: qb_est6: *
7: qb_est7: *
8: qb_est8: *
9: qb_est9: *
10: qb_est10: *
11: qb_est11: *
12: qb_est12: *
13: qb_est13: *
14: qb_est14: *
15: qb_est15: *
16: qb_est16: *
17: qb_est17: *
18: qb_est18: *
19: qb_est19: *
20: qb_est20: *
21: qb_est21: *
22: qb_est22: *
23: qb_est23: *
24: qb_est24: *
25: qb_est31: *
26: qb_est32: *
27: qb_est35: *
28: qb_est36: *
29: qb_est37: *
30: qb_est38: *
31: qb_est39: *
32: qb_est40: *
33: em_estba: *
34: em_estfun: *
35: em_esthum1: *
36: em_esthum2: *
37: em_esthum3: *
38: em_esthum4: *
39: em_esthum5: *
40: em_esthum6: *
41: em_esthum7: *
42: em_esthum8: *
43: em_esthum9: *

44: em_esthum10: *
45: em_esthum11: *
46: em_esthum12: *
47: em_esthum13: *
48: em_esthum14: *
49: em_esthum15: *
50: em_esthum16: *
51: em_esthum17: *
52: em_esthum18: *
53: em_esthum19: *
54: em_esthum20: *
55: em_esthum21: *
56: em_esthum22: *
57: em_esthum23: *
58: em_esthum24: *
59: em_esthum25: *
60: em_esthum26: *
61: em_esthum27: *
62: em_esthum28: *
63: em_estin1: *
64: em_estin2: *
65: em_estin3: *
66: em_estin4: *
67: em_estin5: *
68: em_estin1: *
69: em_estin2: *
70: em_estov1: *
71: em_estov2: *
72: em_estpl1: *
73: em_estpl2: *
74: em_estpl3: *
75: em_estpl4: *
76: em_estpl5: *
77: em_estpl6: *
78: em_estpl7: *
79: em_estpl8: *
80: em_estpl9: *
81: em_estpl10: *
82: em_estro1: *
83: em_estro2: *
84: em_estro3: *
85: em_estro4: *
86: em_estro5: *
87: em_estro6: *
88: em_estro7: *
89: em_estro8: *
90: em_estro9: *
91: em_estro10: *
92: em_estro11: *
93: em_estro12: *
94: em_estro13: *
95: em_estro14: *
96: em_estro15: *
97: em_estro16: *
98: em_estro17: *
99: em_estro18: *
100: em_estro19: *
101: em_estro20: *
102: qb_est25: *
103: qb_est26: *
104: qb_est27: *
105: qb_est28: *
106: qb_est29: *
107: qb_est30: *
108: qb_est31: *
109: qb_est32: *
110: qb_est33: *
111: qb_est34: *
112: qb_est35: *
113: qb_est36: *
114: qb_est37: *
115: qb_est38: *
116: qb_est39: *

117: qb_est48:*
 118: qb_est49:*
 119: qb_est50:*
 120: qb_est51:*
 121: qb_est52:*
 122: qb_est53:*
 123: qb_est54:*
 124: qb_est55:*
 125: qb_est56:*
 126: qb_est57:*
 127: qb_est58:*
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190: qb_est121:*
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 196: qb_est127:*
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 248: qb_est179:*
 249: qb_est180:*
 250: qb_est181:*
 251: qb_est182:*
 252: qb_est183:*
 253: qb_est184:*
 254: qb_est185:*
 255: qb_est186:*
 256: qb_est187:*
 257: qb_est188:*
 258: qb_est189:*

Pred. No. is the number of results predicted by chance to be greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 12 | 100.0 | 46 | 18 | AI250491 |
| 2 | 12 | 100.0 | 69 | 18 | AI250568 |
| 3 | 12 | 100.0 | 76 | 18 | AI250568 |
| 4 | 12 | 100.0 | 85 | 18 | AI250568 |
| 5 | 12 | 100.0 | 97 | 112 | AI174727 |
| 6 | 12 | 100.0 | 88 | 22 | AI581595 |
| 7 | 12 | 100.0 | 88 | 197 | AI581595 |
| 8 | 12 | 100.0 | 91 | 151 | AI581595 |
| 9 | 12 | 100.0 | 94 | 4 | AA261341 |
| 10 | 12 | 100.0 | 96 | 14 | AA261341 |
| 11 | 12 | 100.0 | 103 | 170 | BF978618 |
| 12 | 12 | 100.0 | 106 | 175 | BF248888 |
| 13 | 12 | 100.0 | 109 | 189 | BF248888 |
| 14 | 12 | 100.0 | 111 | 142 | BF248888 |
| 15 | 12 | 100.0 | 112 | 4 | AA212091 |
| 16 | 12 | 100.0 | 113 | 5 | AA212091 |
| 17 | 12 | 100.0 | 113 | 144 | BF090090 |
| 18 | 12 | 100.0 | 115 | 4 | AA234344 |
| 19 | 12 | 100.0 | 116 | 140 | BF248888 |
| 20 | 12 | 100.0 | 124 | 165 | BF241745 |
| 21 | 12 | 100.0 | 125 | 169 | BF080265 |
| 22 | 12 | 100.0 | 127 | 134 | AI191024 |
| 23 | 12 | 100.0 | 131 | 117 | AW534749 |
| 24 | 12 | 100.0 | 132 | 111 | AW063977 |
| 25 | 12 | 100.0 | 136 | 113 | AW237673 |
| 26 | 12 | 100.0 | 136 | 137 | BF554476 |
| 27 | 12 | 100.0 | 136 | 149 | BF248888 |
| 28 | 12 | 100.0 | 138 | 149 | BF248888 |
| 29 | 12 | 100.0 | 142 | 18 | AI130132 |
| 30 | 12 | 100.0 | 144 | 121 | AW821818 |
| 31 | 12 | 100.0 | 144 | 147 | BF375776 |
| 32 | 12 | 100.0 | 146 | 22 | AI591293 |
| 33 | 12 | 100.0 | 146 | 22 | AI130132 |
| 34 | 12 | 100.0 | 149 | 187 | BF248888 |
| 35 | 12 | 100.0 | 151 | 143 | BF248888 |
| 36 | 12 | 100.0 | 154 | 140 | BF248888 |
| 37 | 12 | 100.0 | 155 | 118 | AW574303 |
| 38 | 12 | 100.0 | 158 | 172 | BF081471 |
| 39 | 12 | 100.0 | 159 | 136 | AI000987 |
| 40 | 12 | 100.0 | 160 | 108 | AV001010 |
| 41 | 12 | 100.0 | 160 | 168 | BF192339 |
| 42 | 12 | 100.0 | 161 | 157 | BF081471 |
| 43 | 12 | 100.0 | 162 | 18 | AI111965 |
| 44 | 12 | 100.0 | 162 | 18 | AI111965 |
| 45 | 12 | 100.0 | 163 | 13 | AI130132 |

ALIGNMENTS

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 12 | 100.0 | 46 | 18 | AI250491 |
| 2 | 12 | 100.0 | 69 | 18 | AI250568 |
| 3 | 12 | 100.0 | 76 | 18 | AI250568 |
| 4 | 12 | 100.0 | 85 | 18 | AI250568 |
| 5 | 12 | 100.0 | 97 | 112 | AI174727 |
| 6 | 12 | 100.0 | 88 | 22 | AI581595 |
| 7 | 12 | 100.0 | 88 | 197 | AI581595 |
| 8 | 12 | 100.0 | 91 | 151 | AI581595 |
| 9 | 12 | 100.0 | 94 | 4 | AA261341 |
| 10 | 12 | 100.0 | 96 | 14 | AA261341 |
| 11 | 12 | 100.0 | 103 | 170 | BF978618 |
| 12 | 12 | 100.0 | 106 | 175 | BF248888 |
| 13 | 12 | 100.0 | 109 | 189 | BF248888 |
| 14 | 12 | 100.0 | 111 | 142 | BF248888 |
| 15 | 12 | 100.0 | 112 | 4 | AA212091 |
| 16 | 12 | 100.0 | 113 | 5 | AA212091 |
| 17 | 12 | 100.0 | 113 | 144 | BF090090 |
| 18 | 12 | 100.0 | 115 | 4 | AA234344 |
| 19 | 12 | 100.0 | 116 | 140 | BF248888 |
| 20 | 12 | 100.0 | 124 | 165 | BF241745 |
| 21 | 12 | 100.0 | 125 | 169 | BF080265 |
| 22 | 12 | 100.0 | 127 | 134 | AI191024 |
| 23 | 12 | 100.0 | 131 | 117 | AW534749 |
| 24 | 12 | 100.0 | 132 | 111 | AW063977 |
| 25 | 12 | 100.0 | 136 | 113 | AW237673 |
| 26 | 12 | 100.0 | 136 | 137 | BF554476 |
| 27 | 12 | 100.0 | 136 | 149 | BF248888 |
| 28 | 12 | 100.0 | 138 | 149 | BF248888 |
| 29 | 12 | 100.0 | 142 | 18 | AI130132 |
| 30 | 12 | 100.0 | 144 | 121 | AW821818 |
| 31 | 12 | 100.0 | 144 | 147 | BF375776 |
| 32 | 12 | 100.0 | 146 | 22 | AI591293 |
| 33 | 12 | 100.0 | 146 | 22 | AI130132 |
| 34 | 12 | 100.0 | 149 | 187 | BF248888 |
| 35 | 12 | 100.0 | 151 | 143 | BF248888 |
| 36 | 12 | 100.0 | 154 | 140 | BF248888 |
| 37 | 12 | 100.0 | 155 | 118 | AW574303 |
| 38 | 12 | 100.0 | 158 | 172 | BF081471 |
| 39 | 12 | 100.0 | 159 | 136 | AI000987 |
| 40 | 12 | 100.0 | 160 | 108 | AV001010 |
| 41 | 12 | 100.0 | 160 | 168 | BF192339 |
| 42 | 12 | 100.0 | 161 | 157 | BF081471 |
| 43 | 12 | 100.0 | 162 | 18 | AI111965 |
| 44 | 12 | 100.0 | 162 | 18 | AI111965 |
| 45 | 12 | 100.0 | 163 | 13 | AI130132 |

JOURNAL

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: rstra@fmail.nih.gov

Unknown library type

Trace considered overall poor quality

Insert length: 404 Std Error: 0.00

Seq primer: 400P from Gibco

High quality sequence stop: 1

Insert length/Qualifiers

1: 146

Source

Zygote "Male"

Zygote "Female"

Zygote "Male"

Zygote "Female"

Zygote "Male"

Zygote "Female"

Zygote "Male"

Zygote "Female"

Zygote "Male"

Zygote "Female"

Zygote "Male"

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Zygote "Female"

Zygote "Male"

Zygote "Female"

| | | | | | | | |
|--------------------------|--|------|----------------|---------|---------|------------------------|---------|
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 4 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 5 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 6 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 7 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 8 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 9 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 10 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 11 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 12 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 13 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 14 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 15 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 16 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 17 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 18 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 19 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 20 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |
| DEFINITION | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| TITLE | | | | | | | |
| JOURNAL | | | | | | | |
| COMMENT | | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | | | | | | | |
| BASE COUNT | | 17 a | 12 c | 20 g | 18 t | Non amplified library. | |
| ORIGIN | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity | | | | | | | |
| Matches 12: Conservative | | | | | | | |
| QY | | 1 | CTGAGATGATG 12 | 100.00% | 100.00% | 100.00% | 100.00% |
| DB | | 35 | CTGAGATGATG 46 | 100.00% | 100.00% | 100.00% | 100.00% |
| RESULT 21 | | | | | | | |
| AA554284 | | | | | | | |
| LOCUS | | | | | | | |

[illegible]

| | | | | | | |
|--|--|--|----------|-------------|----|---|
| <hr/> | | | | | | |
| Zclone lib "Cam c104.s" | | | | | | |
| ZAccessType "hypocotyl" and cotinole, germinated seeds" | | | | | | |
| ZLab host "DH10B" | | | | | | |
| ZAuto vector "pT7-3lac (pharmacia)"; Site 1: EcoRI; | | | | | | |
| Site 2: Not I; This cDNA library was constructed from mRNA | | | | | | |
| isolated from hypocotyl and plumule tissues of seeds | | | | | | |
| germinated for three days of the cultivar Williams. | | | | | | |
| Complementary DNA was synthesized from mRNA using a primer | | | | | | |
| consisting of a poly(dI) sequence with a blunt-ended cDNA | | | | | | |
| site. EcoRI adapters were ligated to the blunt-ended cDNA | | | | | | |
| fragments followed by digestion with EcoRI and NotI. The | | | | | | |
| cDNA fragments were directionally cloned into the | | | | | | |
| EcoRI-NotI restriction site of the pT7-3lac vector. The | | | | | | |
| ligated cDNA fragments were transformed into DH10B host | | | | | | |
| cells (Gibco BRL). This library was constructed by Dr. | | | | | | |
| Randy Shoenmaker." | | | | | | |
| WASE C/DNT | 44 | a | 16 | c | 29 | t |
| ORIGIN | | | | | | |
| <hr/> | | | | | | |
| Query Match | 100.0% | Score 12: | DB 17%: | Length 106: | | |
| Best Local Similarity | 100.0% | Prod No: | 1.2e+04: | | | |
| Matches 12: | Conservative 0: | Mismatches 0: | Gaps 0: | | | |
| <hr/> | | | | | | |
| Seq | 1 | CTCAAGATGATG 12 | | | | |
| | | | | | | |
| B | 75 | CTGAAGATGATG 86 | | | | |
| <hr/> | | | | | | |
| DESCRIPTION | 13 | | | | | |
| 94146 | | | | | | |
| KEYWORDS | | | | | | |
| DEFINITION | F52913, cDNA clone IMAGE:119039.5; Similar to db:L21696_cDS1 PEGHYME-STN ALPHA (HUMAN) | | | | | |
| | mRNA sequence. | | | | | |
| ACCESSION | T94146 | | | | | |
| VERSION | T94146.1 | GI:727634 | | | | |
| KEYWORDS | EST. | | | | | |
| SOURCE | Homo sapiens | | | | | |
| ORGANISM | Euphyasac | Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | | | |
| REFERENCE | 1 | (bases 1 to 109) | | | | |
| AUTHORS | Hillier, L., Leighton, G., Becker, M., Bonaldo, M.F., Chipchell, R., | | | | | |
| | Chissoe, S., Dietrich, N., Dinklage, J., Fazel, A., Gish, W., Hawkins, | | | | | |
| | Jr., Hultman, M., Kucaba, T., Lucy, M., Le, M., Le, N., Madis, E., Moore, | | | | | |
| | R.B., Morris, M., Parsons, J., Prange, C., Kirkland, J., Kohring, L., | | | | | |
| | Scheuhammer, K., Soares, M.P., Young, J., Zetterberg, J., Zerkowski, E., | | | | | |
| | Zunderwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M. | | | | | |
| | Generation and analysis of 280,000 human expressed sequence tags | | | | | |
| TITLE | Genome Res. 6 (5), 807-828 (1996) | | | | | |
| JOURNAL | 97044478 | | | | | |
| MEDLINE | Wash. St. Univ. Sch. Med. Med. | | | | | |
| COPYRIGHT | Washington University School of Medicine | | | | | |
| | 4444 Forest Park Parkway, Box 8001, ST. LOUIS, MO 63108 | | | | | |
| | tel: 314.286.1800 | | | | | |
| | fax: 314.286.1810 | | | | | |
| | Email: est.watson,wustl.edu | | | | | |
| | High quality sequence starts: 1 | | | | | |
| | High quality sequence stops: 1 | | | | | |
| | Source: IMAGE Consortium, UNL | | | | | |
| | This clone is available royalty free through UNL; contact the | | | | | |
| | IMAGE Consortium (image@unl.edu) for further information. | | | | | |
| | Trace considered overall poor quality | | | | | |
| | Seq primer: M18pt | | | | | |
| | High quality sequence stop: 1 | | | | | |
| | Location/Annotations | | | | | |
| | 1..109 | | | | | |
| | Organism "Homo sapiens" | | | | | |
| | ZBases 197298 | | | | | |
| | Zdb_xref "taxon:9606" | | | | | |
| | "IMAGE:119039" | | | | | |
| | Zclone lib "SH rat genome map (#93/210)" | | | | | |
| <hr/> | | | | | | |
| FEATURES | | | | | | |
| source | | | | | | |

us-09-479-862-6.rst

Thu Aug 2 10:27:00 2001

27-JUN 1993: 97EP 0404616;
27-JUN-1996: 96EP 0185405;
(HAYB) HAYASHIHARA SEIICHIRO KA:JAKU;
Kurimoto M, Okura T, Torioka K;
WPI: 1998-054914/06,
P-PSDB: AAW47429.
Genomic DNA encoding polypeptide inducing interferon gamma
production - by immuno competent cells, useful to treat v.d. human
malignant tumors or viral diseases
Claim 2: Pages 49-50; 74pp; English.
The present sequence encodes a protein, which induces
interferon-gamma (IFN-gamma) production in immunocompetent cells.
The protein has high biological activity, including enhancing
cytotoxicity of killer cells and inducing killer cell formation,
in addition to inducing IFN-gamma production by immunocompetent
cells when expressed in mammalian cells, facilitating its use in
cells when expressed to treat/prevent, v.d. malignant tumors, viral or
bacterial infections and immune diseases. As it is expressed in
mammalian cells, it also has low toxicity when used in human
treatments, minimising side effects. The DNA encoding the protein
can be used in gene therapy, v.d. by infecting vectors containing
the DNA or transplanting cells.
Sequence 1120 bp; 378 A; 227 C; 241 G; 283 T; 1 other;
Query Match 100.0%; Score 87; 101 bp; Length 1120;
Best Local Similarity 100.0%; Prod. No. 6,7e 19;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATATAATGACTGTCAGACAGAGAGAAATAGATGACACTTCTGCTAAAGAA 60
DB 170 gaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 229
QY 61 TTAATGAAATAGAGTCTTACTTTATAG 87
DB 230 ttattgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 256
RESULT 6
ID AAZ36876
AC AAZ36876;
XX 11-MAR 2000 (first entry)
XX DNA encoding a protein that induces IFN-gamma production.
XX Human; interferon gamma production; IFN-gamma; immunocompetent cell;
XX and viral; immunoregulatory; antiviral; mitogen;
XX IFN-gamma susceptible disease; and bacterial; antitumor;
XX blood bacterial enhancing agent; hepatitis; herpes syndrome; candida;
XX AIDS; bacterial disease; candidiasis; malaria; solid malignant tumor;
XX renal cancer; mycosis tumours; chronic granulomatous disease;
XX blood cell malignant tumor; adult T cell leukemia;
XX chronic myelopneupsis leukemia; malignant leukemia; immune disease;
XX allergy; rheumatism; ds.
XX Homo sapiens.
XX Key location/Qualifiers
FT CDS 1..177
FT /*aa d
FT CDS 178..759
FT /*aa b

/transl_except (pos: 502..504, aa: Xaa)
/auto_xaa is the of the
178..285
/*aa c
286..756
/*aa d
760..1120
/*aa e
XX EP962531 A2.
XX 08 DEC 1993.
XX 10 NOV 1995; 99EP 0104104.
XX 15 NOV 1994; 94IP 0043263.
XX 23 FEB 1995; 95IP 0058240.
XX 10 MAR 1995; 95IP 0078557.
XX 18 SEP 1995; 95IP 0262062.
XX 29 SEP 1995; 95IP 0274988.
XX 10 NOV 1995; 95EP 0080555.
XX (HAYB) HAYASHIHARA SEIICHIRO KA:JAKU.
XX Ushiro S, Torioka K, Yamamoto T, Okamura H.
XX WPI: 2000-064283/06,
XX P-PSDB: AAY5008.
XX Novel polypeptides used in the treatment of interferon gamma
susceptible diseases
XX Example A.4 3: Page 7; 42pp; English.
XX The present sequence encodes a human protein that induces interferon
XX (IFN) gamma production by immunocompetent cells. IFN-gamma is a
XX protein which has antiviral, antitumor and immunoregulatory activity
XX and is produced by immunocompetent cells stimulated with antigenic
XX mitogens. The protein of the invention is used to treat IFN-gamma
XX susceptible diseases, and also have use as a antiviral agent, an
XX antitumor agent, and tumor agent, immunoregulatory agent, and
XX platelet enhancing agent. Diseases which can be treated with the
XX protein include viral diseases such as hepatitis, herpes synde, and
XX condyloma, and AIDS; bacterial diseases such as renal cancer, mycois,
XX malaria; solid malignant tumors such as renal cancer, lymphoma,
XX tumours; and chronic granulomatous disease; blood cell malignant
XX tumors such as adult T cell leukemia; chronic myelopneupsis leukemias
XX and malignant leukemia; and immune diseases such as allergy and
XX rheumatism.
XX Sequence 1120 bp; 378 A; 227 C; 241 G; 283 T; 1 other;
Query Match 100.0%; Score 87; 101 bp; Length 1120;
Best Local Similarity 100.0%; Prod. No. 6,7e 19;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATATAATGACTGTCAGACAGAGAGAAATAGATGACACTTCTGCTAAAGAA 60
DB 170 gaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 229
QY 61 TTAATGAAATAGAGTCTTACTTTATAG 87
DB 230 ttattgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 256
RESULT 6
ID AAZ36876
AC AAZ36876;
XX 11-MAR 2000 (first entry)
XX DNA encoding a protein that induces IFN-gamma production.
XX Human; interferon gamma production; IFN-gamma; immunocompetent cell;
XX and viral; immunoregulatory; antiviral; mitogen;
XX IFN-gamma susceptible disease; and bacterial; antitumor;
XX blood bacterial enhancing agent; hepatitis; herpes syndrome; candida;
XX AIDS; bacterial disease; candidiasis; malaria; solid malignant tumor;
XX renal cancer; mycosis tumours; chronic granulomatous disease;
XX blood cell malignant tumor; adult T cell leukemia;
XX chronic myelopneupsis leukemia; malignant leukemia; immune disease;
XX allergy; rheumatism; ds.
XX Homo sapiens.
XX Key location/Qualifiers
FT CDS 1..177
FT /*aa d
FT CDS 178..759
FT /*aa b

QY 61 JIATPGACAAATGCTTATCTTATAG B7
 ID 15659 Ttataacataacpcttactttatata 15685
 RESULT 9
 ID AAV48228 standard; DNA: 11464 bp
 AC AAV48228;
 XX 16-NOV-1998 (first entry)
 XX Interleukin 18 construct.
 DE Human; interleukin 18; IL18; osteoclast; hypercalcaemia; osteoporosis; ds;
 KW osteoclastoma; Rebert's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity; osteitis; primary hyperthyroidism;
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 3..11446
 FT /*tag a "interleukin 18"
 FT 1..3
 FT /*tag b
 FT 4..82
 FT /*tag c
 FT /note "leader peptide"
 FT 83..1453
 FT /*tag d
 FT /number 1
 FT 1454..1465
 FT /*tag e
 FT /note "leader peptide"
 FT 1466..4848
 FT /*tag f
 FT /number 2
 FT 4849..4865
 FT /*tag g
 FT /note "leader peptide"
 FT 4866..4983
 FT /*tag h
 FT 4984..5317
 FT /*tag i
 FT /number 3
 FT 5318..6451
 FT /*tag j
 FT 6452..11224
 FT /*tag k
 FT /number 4
 FT 11225..11443
 FT /*tag l
 FT 11444..11464
 FT 3'UTR
 XX EP861663 A2.
 FN 02 SEP-1998.
 UD 24 FEB-1998; 98EP-0301452.
 XX 25-FEB-1997; 97JP-0055468.
 XX (HAYASHI) HAYASHIMURA SEIBUISHI KASAKI.
 XX Gillespie MT, Horwood NJ, Kurimoto M, Okada N;
 DR WPT; 1998-448964/99.
 DR F-ESDB; AAW37082.
 XX Use of interleukin-18 to inhibit osteoclast formation in treatment

PI of vcd, hypercalcaemia, osteoclastoma, Rebert's syndrome,
 PI osteosarcoma, chronic rheumatoid arthritis, deformity and/or
 PI primary hyperthyroidism and osteoporosis
 XX Disclonore; Page 24 28; 96pp; English
 XX Interleukin 18 (IL 18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL 18 is used for treatment of
 CC prevention of osteoclast related diseases e.g., hypercalcaemia, ds, ds, ds,
 CC Rebert's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteoporosis and
 CC osteoporosis.
 XX Sequence 11464 bp: 5622 A; 2114 C; 2465 G; 3263 T; 0 other
 SQ
 Query Match 94.9% Score 82; 100 bp; Length 11464
 Best Local Similarity 100.0%; Field No. 4; 100 bp
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Id 0
 QY 6 AAV48228 (AAV48228) AAV48228 (AAV48228) AAV48228 (AAV48228)
 ID 1 AAV48228 (AAV48228) AAV48228 (AAV48228) AAV48228 (AAV48228)
 QY 66 (AAV48228) (AAV48228) (AAV48228) (AAV48228)
 ID 61 AAV48228 (AAV48228) AAV48228 (AAV48228) AAV48228 (AAV48228)
 RESULT 10
 ID AAV18506 standard; cDNA: 579 bp
 AC AAV18506;
 XX 07 JUL 1998 (first entry)
 DE Interferon-gamma inducing precursor peptide cDNA.
 KW Interferon-gamma inducing precursor peptide; IFN gamma; ds;
 KW Interleukin 1 beta-converting enzyme; ICE; cytolysin; killer cell
 KW antiviral agent; antitumor agent; immunoply agent; and isotype
 XX Mammalia.
 OS
 XX Key Location/Qualifiers
 FH CDS 1..579
 FT /*tag a
 FT /product "IFN gamma inducing precursor peptide"
 FT 1..108
 FT /*tag b
 FT 109..579
 FT /*tag c
 FT /product "IFN gamma inducing peptide"
 FN EP941003 A2.
 XX 28 JAN 1998.
 XX 18 JUL 1997; 97EP-0405476.
 XX 31 JAN 1997; 97JP-0041474.
 XX 25 JUL 1996; 96JP-0213267.
 XX (HAYASHI) HAYASHIMURA SEIBUISHI KASAKI.
 XX Kurimoto M, Tanimoto T;
 XX WPT; 1998-0054790.
 XX F-ESDB; AAW37740.
 XX Conversion of interferon inducing polypeptide precursor to a
 PI polypeptide comprises use of interleukin 1 beta-converting enzyme

us-09-479-862-5.rng

Thu Aug 2 10:26:55 2001

QY 1561 CTCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGCTGAGAGAT 1620
 DB 28488 CTCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 28417
 QY 1621 CACTTCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 1680
 DB 28448 CACTTCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 28507
 QY 1681 GCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 1740
 DB 28508 GCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 28567
 QY 1741 TATTCCTGATATGAACTAAATGATCTGAAAGACCTGAAAGACCTGAAAGACCTGAAAGAT 1800
 DB 28568 TATTCCTGATATGAACTAAATGATCTGAAAGACCTGAAAGACCTGAAAGACCTGAAAGAT 28627
 QY 1801 TAAAGACCTGAGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 1860
 DB 28628 TAAAGACCTGAGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 28687
 QY 1861 TTAAGACCTGAGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 1920
 DB 28688 TTAAGACCTGAGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 29747
 QY 1921 CACTTCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 1980
 DB 28748 CACTTCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 28807
 QY 1981 GCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 2040
 DB 28808 GCAGTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 28867
 QY 2041 ACCGAAATGATATGAACTAAATGATCTGAAAGACCTGAAAGACCTGAAAGACCTGAAAGAT 2100
 DB 28868 ACCGAAATGATATGAACTAAATGATCTGAAAGACCTGAAAGACCTGAAAGACCTGAAAGAT 28927
 QY 2101 GTTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 2160
 DB 28928 GTTGGAGATAGCATATACCTTTCAGTAAAGACCTACCTTTCAGAGAGCTGAGAGAT 28987
 QY 2161 ATTACT 2167
 DB 28988 attact 28994
 RESULT 2
 ID AAV05368 standard: cDNA, 1480 bp
 AC AAV05368:
 XX
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE cDNA encoding human interleukin-1-gamma.
 KW Interleukin 1 gamma, IL 1 gamma, mouse cytokine, 321F, which induces certain T cells to produce interferon-gamma. Human IL-1-gamma and mouse 321F show 71% identity at the nucleotide level and approximately 65% identity at the amino acid level. Antagonists of IL-1 gamma, C-3, antibodies, can be used in a method for treating a condition caused by human IL-1 gamma. The antibodies can also be used in diagnostic assays. The IL-1 gamma protein can be covalently conjugated to polyethylene glycol or to a polypeptide, and the fusion protein used in a pharmaceutical composition for supplying the biological activity of IL-1 gamma. Conditions that can be treated using the human IL-1-gamma protein include immunological disorders, allergies, and infectious diseases. The IL-1-gamma can also be used to detect the presence of the protein or its receptor.
 KW Homo sapiens.
 OS Homo sapiens.
 FH
 FH Key Location/Qualifiers
 DB 435..1016
 FT /product= a
 FT /product= interleukin-1-gamma
 PL
 PN WC09744468-A1.
 XX
 XX 27-NOV-1997.
 XX
 XX 16-MAY-1997; 97NC-US07282.
 XX

PK 20-MAY-1996; 96US-0651998.
 XX (SCHE) SCHERING CORP.
 XX
 PI Bazan JF, Hardiman GT, Kastelenin RA, Sana TR, Timans JC;
 DR WPI: 1998 0185223/02.
 DR P-PSDB: AAW46592.
 XX
 XX Antagonist of human interleukin 1 gamma used for treating immunological disorders caused by human IL-1-gamma
 PR
 PS Disclosure; Pages 53-54; 63pp; English.
 XX
 CC The present sequence encodes human interleukin-1-gamma (IL-1-gamma). The protein is the human equivalent of a mouse cytokine, 321F, which induces certain T cells to produce interferon-gamma. Human IL-1-gamma and mouse 321F show 71% identity at the nucleotide level and approximately 65% identity at the amino acid level. Antagonists of IL-1 gamma, C-3, antibodies, can be used in a method for treating a condition caused by human IL-1 gamma. The antibodies can also be used in diagnostic assays. The IL-1 gamma protein can be covalently conjugated to polyethylene glycol or to a polypeptide, and the fusion protein used in a pharmaceutical composition for supplying the biological activity of IL-1 gamma. Conditions that can be treated using the human IL-1-gamma protein include immunological disorders, allergies, and infectious diseases. The IL-1-gamma can also be used to detect the presence of the protein or its receptor.
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 Best Local Similarity 100.0%; Pred. No. 1.5e 78;
 Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 855 agtctccagacatgataataatgaatttgaattctcatcagagagatctt 914
 QY 121 CTACTCTGCAAAAAGACAGACAGCTTTTAAACTCATTTTGAAAAGAGATGAAATG 180
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 DB 1155 atacaaaatatagtgagtgagagatgagagatgagagatgagagatgagagatgag 1214
 QY 421 GAGGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 480
 DB 1215 gaggagatgagagatgagagatgagagatgagagatgagagatgagagatgagag 1274
 QY 481 TTTGGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 540
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[illegible]

[illegible]

Genfore version 4.5
Copyright (c) 1993-2000 Genfore Ltd.

-M nucleic - nucleic search, using sw model

Run: 001 August 2, 2001, 06:08:04 : Search time: 4798.44 seconds
(without alignments)
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Perfect score: 2167
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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us-09-479-862-7.rst

Thu Aug 2 10:27:04 2001

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being predicted
and is derived by analysis of the total score distribution.

[illegible]


```

1 APPLICANT: NAME: KASUSHIKI, KAISHA HAYASHIBARA SEIBUTSU KAGAKU
2 APPLICANT: KENKYUJO
3 APPLICANT: KENKAIZA, Inc.
4 APPLICANT: TANIUCHI, Mutsuko
5 APPLICANT: KINO, Kazuo
6 APPLICANT: KURIMOTO, Masashi
7 TITLE OF INVENTION: NON-IONIC AMBIPHILIC SURFACTANT POLYPEPTIDE
8 TITLE OF INVENTION: WHICH THROUGH INTERFERENCE PROTECTION
9 NUMBER OF SEQUENCES: 9
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Browdy and Neimark
12 STREET: 419 Seventh Street N.W. Ste. 400
13 CITY: Washington
14 STATE: D.C.
15 COUNTRY: USA
16 ZIP: 20004
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC DOS/MS Dos
21 SOFTWARE: Word Perfect Version 5.0
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Browdy, Roger L.
24 REGISTRATION NUMBER: 25,618
25 TELEPHONE: (202) 628-5197
26 TELEFAX: (202) 747-3528
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/08/558,918
29 FILING DATE:
30 CLASSIFICATION:
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US/08/558,919
33 FILING DATE:
34 APPLICATION NUMBER: JP 78,457/95
35 FILING DATE: March 10, 1995
36 APPLICATION NUMBER: JP 271,989/95
37 FILING DATE: September 29, 1995
38 INFORMATION FOR SEQ ID NO: 2:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 471 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: double
43 TOPOLOGY: linear
44 MOLECULE TYPE: cDNA to mRNA
45 ORIGINAL SOURCE:
46 ORGANISM: human
47 INDIVIDUAL ISOLATE: liver
48 FEATURE:
49 NAME/KEY: mat peptide
50 LOCATION: 1..471
51 IDENTIFICATION METHOD: S
52 US-09-479-862-7

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Best local Similarity 100.0% Pred. No. 474-32;
Matches 253; Conservative 0; Mismatches 0; Indels 0;
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15 181 GAGGATAGATGATTAAGTGTGATGTTCAAGGATCAAGGATCAAGGATCAAGGAT 240
16 473 GAGGATAGATGATTAAGTGTGATGTTCAAGGATCAAGGATCAAGGATCAAGGAT 471

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RESULT 14
US-09-479-469A-Z
Sequence 2: Affiliation: US/08/74469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KASUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KENKAIZA, Kakuji
APPLICANT: TANIUCHI, Tadao
APPLICANT: KURIMOTO, Masashi
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS Dos
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,918
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/558,919
FILING DATE:
APPLICATION NUMBER: JP 78,457/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 271,989/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/WORKSHEET NUMBER: TORIGOE=1A
TELEPHONE: (202) 628-5197
TELEFAX: (202) 747-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: human
INDIVIDUAL ISOLATE: liver
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..471
IDENTIFICATION METHOD: S
US-09-479-469A-Z

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Query Match 10.1% Score 219; DB 4; Length 471.
Best local Similarity 100.0% Pred. No. 474-32;
Matches 253; Conservative 0; Mismatches 0; Indels 0;
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10 253 GAAATGAATGCTGCTGATAAATCAAGGATACAAAAAGGAAATATATCTTCACAGA 472
11 61 AGTGTGCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGAT 120
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RESULT 7
US-08-864-324-14
Sequence 14, Application: Request: 1
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: TAKAKURA, FUMI
APPLICANT: KIKUCHI, TORIYUKI
APPLICANT: MASUDA, KUMIHIRO
TITLE OF INVENTION: GENETIC DATA ENCODING AND DECRYPTION VARIABLE
TITLE OF INVENTION: OF INHERITING THE FREQUENCY OF INHERITION
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NUMBERS: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-479-862-3
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE TO OTHER APPLICATIONS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-747-6528
TELEFAX: 202-747-6528
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 20994 base pairs
TYPE: nucleic acid
STANDARDS: Double
TOPOLGY: Linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
ISSUE TYPE: Placenta
FEATURE:
NAME/KEY: 507P
LOCATION: 1..15606
IDENTIFICATION METHOD: F
NAME/KEY: 1946P, part 145
LOCATION: 15607..15685
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NAME/KEY: 1946P, part 145
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NAME/KEY: 1946P
LOCATION: 17569..20994
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NAME/KEY: 1946P, part 145
LOCATION: 20452..20468
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NAME/KEY: 507P, part 145
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LOCATION: 20587..21920
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NAME/KEY: 1946P, part 145

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LOCATION: 21921..22054
IDENTIFICATION METHOD: S
NAME/KEY: 1946P
LOCATION: 22055..226827
IDENTIFICATION METHOD: E
NAME/KEY: 1946P, part 145
LOCATION: 22683..227046
IDENTIFICATION METHOD: S
NAME/KEY: 507P
LOCATION: 22705..22894
IDENTIFICATION METHOD: E
US-08-864-324-14

Query Match: 100.0%, Score: 145, DB: 3, Length: 20994
Best Local Similarity: 100.0%, Prod. No.: 2,40-44
Matches: 145, Mismatches: 0, Labels: 0, Gaps: 0

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DB 20452 ATTGCAATGATTAAG 20586

RESULT 8
US-08-558-818-2
Sequence 8, Application: Request: 1
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT:
APPLICANT: KUNIKATA, Toshio
APPLICANT: KENYUJO
APPLICANT: TANIGUCHI, Mitsuo
APPLICANT: FUKU, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PLASMA MEMBRANE ALBUMIN SEPARATION AND PURIFICATION
TITLE OF INVENTION: WHICH INCLUDES INTERFERON PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NUMBERS: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE TO OTHER APPLICATIONS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-747-6528
TELEFAX: 202-747-6528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 58,246/95
FILING DATE: February 24, 1995
INFORMATION FOR SEQ ID NO: 2:

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 195: cm_qss hom 1: *
 196: cm_qss hom 1: *
 197: cm_qss hom 1: *
 198: cm_qss hom 1: *
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 215: cm_qss hom 1: *
 216: cm_qss hom 1: *
 217: cm_qss hom 1: *
 218: db_est 113: *
 219: db_est 114: *
 220: db_est 115: *
 221: db_est 116: *
 222: db_est 117: *
 223: db_est 118: *
 224: db_est 119: *
 225: db_est 120: *
 226: db_est 121: *
 227: db_est 122: *
 228: db_est 123: *
 229: db_est 124: *
 230: db_est 125: *
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 233: db_est 128: *
 234: db_est 129: *
 235: db_est 130: *
 236: db_est 131: *
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 240: db_est 135: *
 241: db_est 136: *
 242: db_est 137: *
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 250: db_est 145: *
 251: db_est 146: *
 252: db_est 147: *
 253: db_est 148: *
 254: db_est 149: *
 255: db_est 150: *

Prod. No. is the number of results predicted by chance. The score is greater than or equal to the score of the result to be tested, and is derived by analysis of the total score distribution.

Thu Aug 2 10:26:56 2001

us-09-479-862-5.rst

Page 10

QY 9 ATGGCTGCTGAACAGAGAGAGAAATGCAATCTTGCTGCTAAAGAAATTTATTAAC 68
 DB 1 AAGCTGCTGAACAGAGAGAGAAATGCAATCTTGCTGCTAAAGAAATTTATTAAC 60

QY 69 AATAAGCTTTACTTTATTAAG 87
 DB 61 AATAAGCTTTACTTTATTAAG 79

RESULT 7
 US 08-896-501A-5
 : Sequence 5, Application US/896501A
 : Patent No. 5991663

: GENERAL INFORMATION:
 : APPLICANT: TANIMOTO, Masashi
 : APPLICANT: KASUJI KURIMOTO
 : TITLE OF INVENTION: KINETIC RISK REDUCTION LITHIUM ION
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.00
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09-479-862-5
 : FILING DATE: 18-JUL-1997
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 213,267/1994
 : FILING DATE: 25-JUL-1996
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 31,411/1997
 : FILING DATE: 31-JAN-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, Roger L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: TANIMOTO 4
 : TELEPHONE: 202-428-5197
 : TELEFAX: 202-428-5197
 : INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 579 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA to mRNA
 : FEATURE:
 : NAME/KEY: leader peptide
 : LOCATION: 1..108
 : IDENTIFICATION METHOD: S
 : NAME/KEY: mat peptide
 : LOCATION: 109..579
 : IDENTIFICATION METHOD: S
 : US 08-896-501A-5

Query Match 90.8%, Score 79, ID 2, Length 579
 Best Local Similarity 100.0%, Prod. No. 1,660,187
 Matches 79, Conserved 0, Mismatches 0, Indels 0

QY 9 ATGGCTGCTGAACAGAGAGAAATGCAATCTTGCTGCTAAAGAAATTTATTAAC 68
 DB 1 AAGCTGCTGAACAGAGAGAGAAATGCAATCTTGCTGCTAAAGAAATTTATTAAC 60

QY 69 AATAAGCTTTACTTTATTAAG 87
 DB 61 AATAAGCTTTACTTTATTAAG 79

DB 61 AATAAGCTTTACTTTATTAAG 79
 RESULT 8
 US 08-884-424-24
 : Sequence 24, Application US/08884424
 : Patent No. 6060284

: GENERAL INFORMATION:
 : APPLICANT: Takamori OKURA
 : APPLICANT: KASUJI KURIMOTO
 : APPLICANT: Masashi KURIMOTO
 : TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE ZEPHYRIN
 : TITLE OF INVENTION: OF INHERING THE PRODUCTION OF INTERFERON
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.40
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08-884-424
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 3,347,377,96
 : FILING DATE: 27-JUN-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, Roger L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: OKURA 1
 : TELEPHONE: 202-428-5197
 : TELEFAX: 202-428-5197
 : INFORMATION FOR SEQ ID NO: 24:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 33 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US 08-884-424-24

Query Match 47.9%, Score 17, ID 3, Length 33
 Best Local Similarity 100.0%, Prod. No. 0,0044
 Matches 33, Conserved 0, Mismatches 0, Indels 0

QY 41 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 73
 DB 33 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 1

RESULT 9
 US 08-884-424-24
 : Sequence 24, Application US/08884424
 : Patent No. 6060284

: GENERAL INFORMATION:
 : APPLICANT: Takamori OKURA
 : APPLICANT: KASUJI KURIMOTO
 : APPLICANT: Masashi KURIMOTO
 : TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE ZEPHYRIN
 : TITLE OF INVENTION: OF INHERING THE PRODUCTION OF INTERFERON
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.40
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08-884-424
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 3,347,377,96
 : FILING DATE: 27-JUN-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, Roger L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: OKURA 1
 : TELEPHONE: 202-428-5197
 : TELEFAX: 202-428-5197
 : INFORMATION FOR SEQ ID NO: 24:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 33 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US 08-884-424-24

Query Match 47.9%, Score 17, ID 3, Length 33
 Best Local Similarity 100.0%, Prod. No. 0,0044
 Matches 33, Conserved 0, Mismatches 0, Indels 0

QY 41 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 73
 DB 33 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 1

RESULT 9
 US 08-884-424-24
 : Sequence 24, Application US/08884424
 : Patent No. 6060284

: GENERAL INFORMATION:
 : APPLICANT: Takamori OKURA
 : APPLICANT: KASUJI KURIMOTO
 : APPLICANT: Masashi KURIMOTO
 : TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE ZEPHYRIN
 : TITLE OF INVENTION: OF INHERING THE PRODUCTION OF INTERFERON
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.40
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08-884-424
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 3,347,377,96
 : FILING DATE: 27-JUN-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, Roger L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: OKURA 1
 : TELEPHONE: 202-428-5197
 : TELEFAX: 202-428-5197
 : INFORMATION FOR SEQ ID NO: 24:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 33 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US 08-884-424-24

Query Match 47.9%, Score 17, ID 3, Length 33
 Best Local Similarity 100.0%, Prod. No. 0,0044
 Matches 33, Conserved 0, Mismatches 0, Indels 0

QY 41 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 73
 DB 33 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 1

RESULT 9
 US 08-884-424-24
 : Sequence 24, Application US/08884424
 : Patent No. 6060284

: GENERAL INFORMATION:
 : APPLICANT: Takamori OKURA
 : APPLICANT: KASUJI KURIMOTO
 : APPLICANT: Masashi KURIMOTO
 : TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE ZEPHYRIN
 : TITLE OF INVENTION: OF INHERING THE PRODUCTION OF INTERFERON
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.40
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08-884-424
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 3,347,377,96
 : FILING DATE: 27-JUN-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, Roger L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: OKURA 1
 : TELEPHONE: 202-428-5197
 : TELEFAX: 202-428-5197
 : INFORMATION FOR SEQ ID NO: 24:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 33 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US 08-884-424-24

Query Match 47.9%, Score 17, ID 3, Length 33
 Best Local Similarity 100.0%, Prod. No. 0,0044
 Matches 33, Conserved 0, Mismatches 0, Indels 0

QY 41 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 73
 DB 33 CAACCTTCGTGAGAAAGAAATTTATTTGACCAATAC 1


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1 REGISTRATION NUMBER: 54,746
2 REFERENCE CHECK NUMBER: 171279, 818
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (212) 382 0100
5 TELEFAX: (212) 382 0888
6 TELEX: 266925
7 INFORMATION FOR SEQ ID NO: 26:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 713 base pairs
10 TYPE: nucleic acid
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 MOLECULE TYPE: DNA (genomic)
14 HYDROPHILIC: No
15 ANTI-SENSE: No
16 US OR 542,806,26

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Query Match: 27,000; Score: 24; ID: 54; Length: 713
Best Local Similarity: 75,000; Prod. No.: 11;
Matches: 40; Conservative: 0; Mismatches: 10; Indels: 0; Gaps: 0;

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01 12 GCTGTCAGCAGTAAAGAAATGATGAACTTCTGGG
06 111 111 111 111 111 111 111 111 111
06 476 ATGCTTATGAAATCAAAATATTTGATGAACTTCTGGG

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Search completed: August 2, 2001, 03:12:40
Job Time: 7646 sec

Genforce version 4.5.

Copyright (c) 1993 - 2000 Compugen Ltd.

CM nucleotide = nucleotide search using sw model

Run on: August 2, 2001, 07:12:21 : Search time: 6699.11 seconds

(without alignments)

50,178 Million cell updates/sec

Filter: US-09-479-862-6

Perfect score: 12

Sequence: 1-17:GAAGATGAG 12

Scoring table: IDENTIFY_NRC

Gapop 10.0 / Gapext 1.0

Searched: 144157 seqs, 773674588 residues

Total number of hits satisfying chosen parameters: 2008414

Minimum db seq length: 0

Maximum db seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEnt1: *

- 1: qb_bal: *
- 2: qb_bal2: *
- 3: qb_bal3: *
- 4: qb_bal4: *
- 5: qb_bal5: *
- 6: qb_bal6: *
- 7: qb_bal7: *
- 8: qb_bal8: *
- 9: qb_bal9: *
- 10: qb_bal10: *
- 11: qb_bal11: *
- 12: qb_bal12: *
- 13: qb_bal13: *
- 14: qb_bal14: *
- 15: qb_bal15: *
- 16: qb_bal16: *
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- 18: qb_bal18: *
- 19: qb_bal19: *
- 20: qb_bal20: *
- 21: qb_bal21: *
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- 23: qb_bal23: *
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- 25: qb_bal25: *
- 26: qb_bal26: *
- 27: qb_bal27: *
- 28: qb_bal28: *
- 29: qb_bal29: *
- 30: qb_bal30: *
- 31: qb_bal31: *
- 32: qb_bal32: *
- 33: qb_bal33: *
- 34: qb_bal34: *
- 35: qb_bal35: *
- 36: qb_bal36: *
- 37: qb_bal37: *
- 38: qb_bal38: *
- 39: qb_bal39: *
- 40: qb_bal40: *
- 41: qb_bal41: *
- 42: qb_bal42: *
- 43: qb_bal43: *

44: qb_bal44: *

45: qb_bal45: *

46: qb_bal46: *

47: qb_bal47: *

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80: qb_bal80: *

81: qb_bal81: *

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89: qb_bal89: *

90: qb_bal90: *

91: qb_bal91: *

92: qb_bal92: *

93: qb_bal93: *

94: qb_bal94: *

95: qb_bal95: *

96: qb_bal96: *

97: qb_bal97: *

98: qb_bal98: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being produced, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB ID | Description |
|------------|-------|-------|--------|-------|-------------|
| | | Match | Length | | |
| 1 | 12 | 100.0 | 12 | 10 | 115645 |
| 2 | 12 | 100.0 | 19 | 9 | AR02040 |
| 3 | 12 | 100.0 | 20 | 9 | AR056084 |
| 4 | 12 | 100.0 | 20 | 10 | 125425 |
| 5 | 12 | 100.0 | 25 | 9 | AR056083 |
| 6 | 12 | 100.0 | 25 | 9 | AR059145 |
| 7 | 12 | 100.0 | 25 | 10 | 125424 |
| 8 | 12 | 100.0 | 54 | 9 | AR036045 |

[illegible]

APPENDIX IV

[illegible]

```

Query Match      100.0%  Score 12; DB 9; Length 25;
Best Local Similarity 100.0%  Pred. No. 6,600.0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGATGAG 12
ID 12 CTGAAGATGAG 1

RESULT 4
LOCALS
125425/c
DEFINITION
Sequence 1 from Patent US 5847854.
ACCESSION
AR059083.1 GI:5984722
VERSION
125425.1 GI:1605294
KEYWORDS
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Mulder, C.
TITLE
Oligonucleotides with anti-Epstein-Barr virus activity
JOURNAL
Patent: US 5847854-A 2 27-AUG-1996;
FEATURES
Location/Qualifiers
1..25
/organism "unknown"
BASE COUNT      8 a 5 c 2 g 5 t
ORIGIN

Query Match      100.0%  Score 12; DB 10; Length 20;
Best Local Similarity 100.0%  Pred. No. 6,600.0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGATGAG 12
ID 12 CTGAAGATGAG 1

RESULT 5
LOCALS
AR059083
DEFINITION
Sequence 1 from Patent US 5847854.
ACCESSION
AR059083
VERSION
AR059083.1 GI:5984660
KEYWORDS
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Mulder, C.
TITLE
Oligonucleotides with anti-Epstein-Barr virus activity
JOURNAL
Patent: US 5847854-A 1 17-NOV-1996;
FEATURES
Location/Qualifiers
1..25
/organism "unknown"
BASE COUNT      6 a 6 c 5 g 8 t
ORIGIN

Query Match      100.0%  Score 12; DB 9; Length 25;
Best Local Similarity 100.0%  Pred. No. 6,600.0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGATGAG 12
ID 20 CTGAAGATGAG 9

RESULT 6
LOCALS
AR059145
DEFINITION
Sequence 12 From Patent W00061768.
ACCESSION
AX039045
VERSION
AX039045.1 GI:1122842
KEYWORDS
Human.
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 54)
AUTHORS
Graham, P., Robinson, M., Liu, B., Novick, D., and Blumberg, P.
TITLE
Preparation of biologically active molecules
JOURNAL
Patent: W0 0061768-A 12 19-OCT-2000;
ORIGIN
GRAHAM, PETER (GB) ; ROBINSON, MURRAY (GB) ; LIU, BING (US) ;

```

```

DEFINITION
Sequence 63 from patent US 5847854.
ACCESSION
AR059145
VERSION
AR059145.1 GI:5984722
KEYWORDS
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Mulder, C.
TITLE
Oligonucleotides with anti-Epstein-Barr virus activity
JOURNAL
Patent: US 5847854-A 6 17-NOV-1996;
FEATURES
Location/Qualifiers
1..25
/organism "unknown"
BASE COUNT      8 a 5 c 6 g 6 t
ORIGIN

Query Match      100.0%  Score 12; DB 9; Length 25;
Best Local Similarity 100.0%  Pred. No. 6,600.0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGATGAG 12
ID 12 CTGAAGATGAG 17

RESULT 7
LOCALS
125424/c
DEFINITION
Sequence 1 from Patent US 5550047.
ACCESSION
125424
VERSION
125424.1 GI:1605294
KEYWORDS
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Mulder, C.
TITLE
Oligonucleotides with anti-Epstein-Barr virus activity
JOURNAL
Patent: US 5550047-A 1 27-AUG-1996;
FEATURES
Location/Qualifiers
1..25
/organism "unknown"
BASE COUNT      6 a 6 c 5 g 8 t
ORIGIN

Query Match      100.0%  Score 12; DB 10; Length 25;
Best Local Similarity 100.0%  Pred. No. 6,600.0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGATGAG 12
ID 20 CTGAAGATGAG 9

RESULT 8
LOCALS
AX039045
DEFINITION
Sequence 12 From Patent W00061768.
ACCESSION
AX039045
VERSION
AX039045.1 GI:1122842
KEYWORDS
Human.
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 54)
AUTHORS
Graham, P., Robinson, M., Liu, B., Novick, D., and Blumberg, P.
TITLE
Preparation of biologically active molecules
JOURNAL
Patent: W0 0061768-A 12 19-OCT-2000;
ORIGIN
GRAHAM, PETER (GB) ; ROBINSON, MURRAY (GB) ; LIU, BING (US) ;

```


Fukuyama; *Mollusca*; *chordata*; *Cnidaria*; *Vertebrata*; *Euteleostomi*; *Mammalia*; *Primates*; *Carabini*; *Hominiidae*; *Homo*.

QY 1 AATAAGACGCGGAGCAATATTATTATAGAGATAGATAGAAATAGAGAGAGAGAGTA 60
DB 119 AATAGGACGCGGAGCAATATTATTATAGAGATAGATAGAAATAGAGAGAGAGTA 178
QY 61 TGGTGTAACTAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 179 TGCTGTAACTAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
QY 121 TTATTCCTTTAAG 134
DB 239 TTATTCCTTTAAG 252

RESULT 7
US-08-896-605A-7
: Sequence 7, Application US/08896605A
: Patent No. 5879942
: GENERAL INFORMATION:
: APPLICANT: TANIMOTO, Tadao
: APPLICANT: KURIMOTO, Masashi
: TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08896605A
: FILING DATE: 18 JUL 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 207 691/1996
: FILING DATE: 19-JUL-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 41,474/1997
: FILING DATE: 30 MAY 1997
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/BOOKET NUMBER: TANIMOTO-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-747-3528
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: leader peptide
: LOCATION: 1..108
: IDENTIFICATION METHOD: S
: NAME/KEY: mat peptide
: LOCATION: 109..579
: IDENTIFICATION METHOD: S
US-08-896-605A-7

Query Match 99.7% Score 132.6 DB 2 Length 579
Best Local Similarity 99.3% Pred. No. 1,4e-34
Matches 133, Conservative 1, Mismatches 0, Indels 0, Gaps 0
QY 1 AATAAGACGCGGAGCAATATTATTATAGAGATAGATAGAAATAGAGAGAGAGTA 60

DB 227 AATAAGACGCGGAGCAATATTATTATAGAGATAGATAGAAATAGAGAGAGAGTA 199
QY 61 TGGTGTAACTAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 179 TGCTGTAACTAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
QY 121 TTATTCCTTTAAG 134
DB 347 TTATTCCTTTAAG 360

RESULT 8
US-08-896-501A-5
: Sequence 5, Application US/08896501A
: Patent No. 5891664
: GENERAL INFORMATION:
: APPLICANT: TANIMOTO, Tadao
: APPLICANT: KURIMOTO, Masashi
: TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08896501A
: FILING DATE: 18-JUL-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 213,267,1996
: FILING DATE: 25-JUL-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 41,474/1997
: FILING DATE: 31-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/BOOKET NUMBER: TANIMOTO-3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-747-3528
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: leader peptide
: LOCATION: 1..108
: IDENTIFICATION METHOD: S
: NAME/KEY: mat peptide
: LOCATION: 109..579
: IDENTIFICATION METHOD: S
US-08-896-501A-5

Query Match 99.7% Score 132.6 DB 2 Length 579
Best Local Similarity 99.3% Pred. No. 1,4e-34
Matches 133, Conservative 1, Mismatches 0, Indels 0, Gaps 0
QY 1 AATAAGACGCGGAGCAATATTATTATAGAGATAGATAGAAATAGAGAGAGAGTA 60
DB 227 AATAAGACGCGGAGCAATATTATTATAGAGATAGATAGAAATAGAGAGAGAGTA 200


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1 PRIOR APPLICATION DATA
2 1. APPLICATION NUMBER: 08/099,999,979
3 FILING DATE:
4 APPLICATION NUMBER: 08/099,999,979
5 FILING DATE: March 10, 1995
6 APPLICATION NUMBER: 08/099,999,979
7 FILING DATE: September 29, 1995
8 APPLICATION NUMBER: 08/099,999,979
9 FILING DATE: September 29, 1995
10 NAME: Browdy, Robert L.
11 REGISTRATION NUMBER: 25,618
12 REFERENCE/DECKET NUMBER: 08/099,999,979
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (202) 628-5197
15 TELEFAX: (202) 737-5528
16 INFORMATION FOR SEQ ID NO: 6:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 471 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: double
21 TOPOLOGY: linear
22 MOLECULE TYPE: cDNA to mRNA
23 ORIGINAL SOURCE:
24 ORGANISM: mouse
25 INDIVIDUAL ISOLATE: liver
26 FEATURE:
27 NAME/KEY: 1.471
28 LOCATION: 1.471
29 IDENTIFICATION METHOD: S
30 US-09 971-169A-6

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Query Match: 56.4% Score 75.6; DB 4; Length 471;
Best Local Similarity: 72.7% Prod. No. 6, re-16;
Matches: 96; Conservative: 1; Mismatches: 35; Indels: 0; Gaps: 0;
QY 3 AATGACCCGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 62
DB 118 AGTGAACCCGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 177
QY 63 GTCGACGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 122
DB 178 GTCGACGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 247
QY 123 ATTTCCTTTAAG 134
DB 238 ATTTCCTTTAAG 249

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RESULT 15
US-09 832-180-4
1 Sequence 3, Application 08/099,999,979
2 Patent No. 6,214,584
3 GENERAL INFORMATION:
4 APPLICANT: KAGOSHIMA KAWA-RIKAKO SAKURAI
5 APPLICANT: KENKYOJO
6 APPLICANT: USHIO, Shimpai
7 APPLICANT: TORIGOE, Kakuji
8 APPLICANT: TANIMOTO, Tadao
9 APPLICANT: OKAMURA, Haruki
10 APPLICANT: KURIMOTO, Masashi
11 TITLE OF INVENTION: INTERFERON PRODUCTION METHOD
12 TITLE OF INVENTION: POLYPEPTIDE
13 NUMBER OF SEQUENCES: 14
14 CORRESPONDENCE ADDRESS:
15 ADDRESSEE: Browdy and Naimark
16 STREET: 419 Seventh Street N.W. Ste. 400
17 CITY: Washington
18 STATE: D.C.
19 COUNTRY: USA
20 ZIP: 20004
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: Floppy disk
23 COMPUTER: IBM PC compatible

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1 OPERATING SYSTEM: 10/10/MS-DOS
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: 08/099,999,979
4 FILING DATE:
5 APPLICATION NUMBER: 08/099,999,979
6 FILING DATE: September 29, 1995
7 APPLICATION NUMBER: 08/099,999,979
8 FILING DATE: September 29, 1995
9 APPLICATION NUMBER: 08/099,999,979
10 FILING DATE: September 29, 1995
11 NAME: Browdy, Robert L.
12 REGISTRATION NUMBER: 25,618
13 REFERENCE/DECKET NUMBER: 08/099,999,979
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (202) 628-5197
16 TELEFAX: (202) 737-5528
17 INFORMATION FOR SEQ ID NO: 4:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 471 base pairs
20 TYPE: nucleic acid
21 STRANDEDNESS: double
22 TOPOLOGY: linear
23 MOLECULE TYPE: cDNA to mRNA
24 HYPOCHLORITE: No
25 ANTI-SENSE: No
26 ORIGINAL SOURCE:
27 ORGANISM: mouse
28 TISSUE TYPE: liver
29 FEATURE:
30 NAME/KEY: 1.471 mat peptide
31 IDENTIFICATION METHOD: S
32 US-09 832-180-4

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Query Match: 56.4% Score 75.6; DB 4; Length 471;
Best Local Similarity: 72.7% Prod. No. 6, re-16;
Matches: 96; Conservative: 1; Mismatches: 35; Indels: 0; Gaps: 0;
QY 3 AATGACCCGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 62
DB 118 AGTGAACCCGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 177
QY 63 GTCGACGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 122
DB 178 GTCGACGAGGAGATATTTATTATTAAGTATGATTAAGATAGAGATAGAGATAG 247
QY 123 ATTTCCTTTAAG 134
DB 238 ATTTCCTTTAAG 249

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Search completed: August 2, 2001, 07:12:36
Job time: 764.2 sec

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Genome version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Molecule nucleic search, using sw model

Run on: August 2, 2001, 07:11:39 : Search time: 699.11 seconds
(without alignments)
64,789 Million cell updates/sec

Title: US 09-479-862-5
Perfect score: 87

Sequence: 1 GATATAAGATGAGTTCCTGAATAAATAGCTTACTTATATAG 87

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 184157 seqs, 77897498 residues

Total number of hits satisfying chosen parameters: 2000414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl: *
1: qb_ba1: *
2: qb_ba2: *
3: qb_ba3: *
4: qb_ba4: *
5: qb_ba5: *
6: qb_ba6: *
7: qb_ba7: *
8: qb_ba8: *
9: qb_ba9: *
10: qb_ba10: *
11: qb_ba11: *
12: qb_ba12: *
13: qb_ba13: *
14: qb_ba14: *
15: qb_ba15: *
16: qb_ba16: *
17: qb_ba17: *
18: qb_ba18: *
19: qb_ba19: *
20: qb_ba20: *
21: qb_ba21: *
22: qb_ba22: *
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91: qb_sg39: *
92: qb_sg40: *
93: qb_sg41: *
94: qb_sg42: *
95: qb_sg43: *
96: qb_sg44: *
97: qb_sg45: *
98: qb_sg46: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query Match | Length | ID | Description |
|--------|-----|-------|-------------|--------|----------|----------------------|
| 1 | 87 | 100.0 | 87 | 10 | E15644 | E15644 Homo sapien |
| 2 | 87 | 100.0 | 1102 | 91 | D49950 | D49950 Homo sapien |
| 3 | 87 | 100.0 | 1120 | 10 | E14759 | E14759 Homo sapien |
| 4 | 87 | 100.0 | 1120 | 10 | E15641 | E15641 Homo sapien |
| 5 | 87 | 100.0 | 1120 | 45 | E11745 | E11745 Homo sapien |
| 6 | 87 | 100.0 | 28994 | 10 | E15653 | E15653 Homo sapien |
| 7 | 87 | 100.0 | 164655 | 83 | AB002884 | AB002884 Homo sapien |
| 8 | 87 | 100.0 | 162065 | 73 | AB002883 | AB002883 Homo sapien |

[illegible]

ORIGIN

Query Match 100.0% Score 87: DB 10: Length 1120
 Best Local Similarity 100.0% Pred. No. 8,40-167
 Matches 87: Conservative 0: Mismatches 0: Indels 0

QY 1 GAATAAAGATGGTGGTGAACAGAGAGAGAAATTCATTAAG 60
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 DB 170 GAATAAAGATGGTGGTGAACAGAGAGAGAAATTCATTAAG 60
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QY 61 TTATGACAAATAGCTTACTTATAG 87
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 DB 230 TTATGACAAATAGCTTACTTATAG 256
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RESULT 4
 E14759
 LOCUS Human mRNA for interferon-gamma inducing protein, complete cds
 DEFINITION E14759
 ACCESSION E14759
 VERSION E14759
 KEYWORDS 1998080286-A/1
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Chordata; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; (bases 1 to 1120)
 AUTHORS Ushio, S., Torioka, F., Tanimoto, I., Okamoto, H., and Katamoto, M.
 TITLE POLYPEPTIDE INDUCING PRODUCTION OF INTERFERON GAMMA
 JOURNAL Patent: JP 199807699-A 1 14 JAN 1998
 HAYASHIWARA BIOTECH LAB INC
 COMMENT OS Homo sapiens (human)
 PN JP 199807699-A/1
 PD 13-JAN-1998
 PE 18-SEP-1995 JP 1997030647
 PR 15-NOV-1994 JP 94P 304239
 PT USHIO SHIGEHITO, TORIOKA FUMIO, TANIMOTO IKAHO, OKAMOTO HARUHIKO, KATAMOTO MASASHI
 P2 0376147, 0376148, 0376149, 0376150, 0376151, 0376152, 0376153, 0376154, 0376155, 0376156, 0376157, 0376158, 0376159, 0376160, 0376161, 0376162, 0376163, 0376164, 0376165, 0376166, 0376167, 0376168, 0376169, 0376170, 0376171, 0376172, 0376173, 0376174, 0376175, 0376176, 0376177, 0376178, 0376179, 0376180, 0376181, 0376182, 0376183, 0376184, 0376185, 0376186, 0376187, 0376188, 0376189, 0376190, 0376191, 0376192, 0376193, 0376194, 0376195, 0376196, 0376197, 0376198, 0376199, 0376200, 0376201, 0376202, 0376203, 0376204, 0376205, 0376206, 0376207, 0376208, 0376209, 0376210, 0376211, 0376212, 0376213, 0376214, 0376215, 0376216, 0376217, 0376218, 0376219, 0376220, 0376221, 0376222, 0376223, 0376224, 0376225, 0376226, 0376227, 0376228, 0376229, 0376230, 0376231, 0376232, 0376233, 0376234, 0376235, 0376236, 0376237, 0376238, 0376239, 0376240, 0376241, 0376242, 0376243, 0376244, 0376245, 0376246, 0376247, 0376248, 0376249, 0376250, 0376251, 0376252, 0376253, 0376254, 0376255, 0376256, 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Human sapiens chromosome 11 clone SP11-456J5 map 11p, WORMBASE

SEQUENCE, 19 unordered pieces.

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Arbitrary gaps between the contigs are represented as

contigs of 100 bp, the exact sizes of the gaps are unknown

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 28622 contig of 28622 bp in length

28723 contig of 100 bp in length

28724 contig of 2982 bp in length

52705 52804 gap of 100 bp

52805 68137 contig of 15333 bp in length

68138 68237 gap of 100 bp

68238 79839 contig of 11602 bp in length

79840 79939 gap of 100 bp

79940 90772 contig of 10835 bp in length

90773 90873 gap of 100 bp in length

90874 103693 contig of 12821 bp in length

103694 103793 gap of 100 bp

103794 113917 contig of 10123 bp in length

113918 114017 gap of 100 bp

114115 123325 contig of 8952 bp in length

123326 123709 gap of 100 bp

123710 123723 contig of 6863 bp in length

123724 123725 gap of 100 bp

123726 135892 contig of 6130 bp in length

135893 135894 gap of 100 bp

135895 135896 contig of 4147 bp in length

135897 140149 gap of 100 bp

140150 144259 contig of 4110 bp in length

144260 144359 gap of 100 bp

144360 148078 contig of 3719 bp in length

148079 148178 gap of 100 bp

148179 152182 contig of 4004 bp in length

152183 152293 gap of 100 bp

152294 155213 contig of 2931 bp in length

155214 155313 gap of 100 bp

155314 158714 contig of 3401 bp in length

158715 158814 gap of 100 bp

158815 161423 contig of 2609 bp in length

161424 161523 gap of 100 bp

161524 162742 contig of 1219 bp in length

162743 162842 gap of 100 bp

162843 164655 contig of 1813 bp in length.

164656 164655

Organization: "Homo sapiens"

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26909 AAGAGGAAATTTGAACTCTATGATACGAGAGGAAATTTTCTAGCTTGGA 26958
128 uLysGluArqAspLeuPheCysIleLeuLysLysGluAspGluDom3 145
|||||
26959 AAAAGAGAGAGAGCTTTTAAAGTCTATTGAGAAAGAGAGATGAAATCT 27008
145 LyAspAlaSerHleMetPheIleValGluAsnGluAsp 157
|||||
27009 GAGATAGATCTATATGCTTATCTGTTCAAAAGGAGAGAT 27046
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SEARCH REQUEST FORM

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 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

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|--|--------------------------|-----------------------------------|
| Searcher: <u>Toby Port</u> | NA Sequence (#) <u>6</u> | STN _____ |
| Searcher Phone #: <u>308-3531</u> | AA Sequence (#) _____ | Dialog _____ |
| Searcher Location _____ | Structure (#) _____ | Questel Orbit _____ |
| Date Searcher Picked Up: <u>8/1</u> | Bibliographic _____ | Dr Link _____ |
| Date Completed: <u>8/3</u> | Litigation _____ | Lexis/Nexis _____ |
| Searcher Prep & Review Time: <u>10</u> | Fulltext _____ | Sequence Systems <u>cg</u> |
| Clerical Prep Time _____ | Patent Family _____ | WWW/Internet _____ |
| Online Time: <u>10</u> | Other _____ | Other (specify) _____ |

